

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 05:31:51 ; Search time 1963.49 seconds
(Without alignments)
373.024 Million cell updates/sec

Title: US-09-927-267-13
Perfect score: 35
Sequence: 1 catgctagaatgagatggggtcactctgacact 35

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 843946

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl:*

1:	gb_ba:*
2:	gb_htg:*
3:	gb_in:*
4:	gb_om:*
5:	gb_ov:*
6:	gb_pat:*
7:	gb_ph:*
8:	gb_pl:*
9:	gb_pr:*
10:	gb_ro:*
11:	gb_sts:*
12:	gb_sy:*
13:	gb_un:*
14:	gb_vl:*
15:	em_ba:*
16:	em_fun:*
17:	em_hum:*
18:	em_in:*
19:	em_mu:*
20:	em_om:*
21:	em_or:*
22:	em_ov:*
23:	em_pat:*
24:	em_ph:*
25:	em_pl:*
26:	em_ro:*
27:	em_sts:*
28:	em_un:*
29:	em_vl:*
30:	em_htg_hum:*
31:	em_htg_inv:*
32:	em_htg_other:*
33:	em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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1	18.6	53.1	77	11	G33119	G33119 Ey7976L Hu
2	17.6	50.3	51	6	AX157589	AX157589 Sequence
3	17.6	50.3	51	6	AX157591	AX157591 Sequence
4	17.2	49.1	38	6	AR120506	AR120506 Sequence
5	17.2	49.1	75	9	HS444350	AJ344350 Homo sapi
6	17.2	49.1	88	9	HS162105	X93613 H.sapiens g
7	17.2	49.1	100	9	HUMIGDM	M36099 Human Ig re
8	16.8	48.0	42	6	AR035931	AR035931 Sequence
9	16.8	48.0	42	6	I20167	I20167 Sequence 12
10	16.8	48.0	88	9	HUMIGHB1	M20417 Human agamm
11	16.6	47.4	38	6	AX343247	AX343247 Sequence
12	16.6	47.4	38	6	AX351627	AX351627 Sequence
13	16.2	46.3	36	6	AX078705	AX078705 Sequence
14	16.2	46.3	36	6	AX078728	AX078728 Sequence
15	16.2	46.3	36	6	AX078730	AX078730 Sequence
16	16.2	46.3	36	6	AX078732	AX078732 Sequence
17	16.2	46.3	53	6	AX328132	AX328132 Sequence
18	16	45.7	51	6	AX157590	AX157590 Sequence
19	16	45.7	51	6	AX157592	AX157592 Sequence
20	15.8	44.6	75	6	AR021196	AR021196 Sequence
21	15.6	44.6	60	6	AX350303	AX350303 Sequence
22	15.4	44.0	51	6	AX159286	AX159286 Sequence
23	15.4	44.0	80	6	AX286077	AX286077 Sequence
24	15.4	44.0	81	6	I19306	I19306 Sequence 78
25	15.4	44.0	100	3	URDRRE03	M81025 Urodacus ho
26	15.4	43.4	100	6	AR142897	AR142897 Sequence
27	15.2	43.4	76	9	S75425519	S75462 collagen ty
28	15.2	43.4	79	9	HS444349	AJ344349 Homo sapi
29	15	42.9	32	6	I23375	I23375 Sequence 8
30	15	42.9	32	6	I33277	I33277 Sequence 8
31	15	42.9	38	6	AX343248	AX343248 Sequence
32	15	42.9	38	6	AX351628	AX351628 Sequence
33	15	42.9	51	6	AX116241	AX116241 Sequence
34	15	42.9	56	9	HUMMTCOF02	UB4641 Human putat
35	15	42.9	70	9	AF218354	AF218354 Homo sapi
36	14.8	42.3	51	6	AX161098	AX161098 Sequence
37	14.8	42.3	58	6	AX202483	AX202483 Sequence
38	14.8	42.3	59	6	HUMTCRVJ49	I39587 Homo sapien
39	14.8	42.3	60	6	A29432	A29432 sequence ex
40	14.6	41.7	21	6	AR081624	AR081624 Sequence
41	14.6	41.7	21	6	I29089	I29089 Sequence 10
42	14.6	41.7	21	6	I42136	I42136 Sequence 10
43	14.6	41.7	46	6	AX214195	AX214195 Sequence
44	14.6	41.7	46	6	AX214201	AX214201 Sequence
45	14.6	41.7	46	6	AX214207	AX214207 Sequence
46	14.6	41.7	46	6	AX214213	AX214213 Sequence
47	14.6	41.7	47	6	AX214208	AX214208 Sequence
48	14.6	41.7	50	6	AX147411	AX147411 Sequence
49	14.6	41.7	50	6	AX165859	AX165859 Sequence
50	14.6	41.7	51	6	AR086655	AR086655 Sequence
51	14.6	41.7	51	6	AR086671	AR086671 Sequence
52	14.6	41.7	51	6	AX162069	AX162069 Sequence
53	14.6	41.7	78	10	MUSMTRACA	M36862 Mouse mitoc
54	14.6	41.7	91	6	AX089708	AX089708 Sequence
55	14.6	41.7	91	6	AX089709	AX089709 Sequence
56	14.6	41.7	91	6	AX090163	AX090163 Sequence
57	14.6	41.7	91	6	AX090164	AX090164 Sequence
58	14.6	41.7	95	6	AX044421	AX044421 Sequence
59	14.6	41.7	95	6	AX044422	AX044422 Sequence
60	14.4	41.1	39	6	I27074	I27074 Sequence 16
61	14.4	41.1	47	6	AX194727	AX194727 Sequence
62	14.4	41.1	48	6	AX055382	AX055382 Sequence
63	14.4	41.1	48	6	AX098391	AX098391 Sequence
64	14.4	41.1	51	6	AX156888	AX156888 Sequence
65	14.4	41.1	51	6	AX165610	AX165610 Sequence
66	14.4	41.1	60	6	E40781	E40781 Antihuman F
67	14.4	41.1	66	6	AX231582	AX231582 Sequence
68	14.4	41.1	71	12	XU074372	U74372 Synthetic c
69	14.4	41.1	100	9	HUMCHRP02	L11321 Homo sapien
70	14.4	41.1	100	11	G32510	G32510 A009F33 Hum
71	14.2	40.6	30	6	AX021165	AX021165 Sequence
72	14.2	40.6	51	6	AX190168	AX190168 Sequence
73	14.2	40.6	85	9	HUMIGCAA	J00235 Human Ig ge

C	74	14	40.0	31	6	BD002521	BD002521 Gene comp	147	13.4	38.3	90	6	AX052940	AX052940 Sequence
C	75	14	40.0	33	6	AX004519	G38812 TA8 Plasmid	148	13.4	38.3	94	11	G38812	G38812 TA8 Plasmid
C	76	14	40.0	73	5	CARN2BD8	Z18729 Chlamydozel	149	13.4	38.3	95	11	HSPE14A08	AJ0033613 H.sapiens
C	77	14	40.0	79	6	AR062559	Sequence	150	13.4	38.3	100	9	AJ8122	AJ008122 Homo sapi
C	78	14	40.0	79	6	AR125962	Sequence	151	13.4	38.3	100	12	SYNMISIGDC	MJ2053 Mouse Ig de
C	79	14	40.0	79	6	I47282	Sequence	152	13.2	37.7	20	6	AR002301	AR002301 Sequence
C	80	14	40.0	79	8	PKU240499	Physconia	153	13.2	37.7	20	6	AR053152	AR053152 Sequence
C	81	14	40.0	81	14	AF227771	Hepatitis	154	13.2	37.7	20	6	AR053152	AR053152 Sequence
C	82	14	40.0	82	3	PCGHOMEO	L19179 Phagocata w	155	13.2	37.7	20	6	AR171473	AR171473 Sequence
C	83	14	40.0	86	6	AR042768	Sequence	156	13.2	37.7	21	6	AR171644	AR171644 Sequence
C	84	14	40.0	96	6	A23312	A23312 oligonucleot	157	13.2	37.7	21	6	AR112357	AR112357 Sequence
C	85	14	40.0	96	6	AR013739	Sequence	158	13.2	37.7	21	6	AR163672	AR163672 Sequence
C	86	13.8	39.4	30	6	AR077753	Sequence	159	13.2	37.7	21	6	AX048866	AX048866 Sequence
C	87	13.8	39.4	31	6	AX053547	Sequence	160	13.2	37.7	23	6	AR003588	AR003588 Sequence
C	88	13.8	39.4	44	6	AX343236	Sequence	161	13.2	37.7	25	6	A46987	A46987 Sequence
C	89	13.8	39.4	44	6	AX353884	Sequence	162	13.2	37.7	27	6	AR102350	AR102350 Sequence
C	90	13.8	39.4	50	6	AR032920	Sequence	163	13.2	37.7	28	6	AX052685	AX052685 Sequence
C	91	13.8	39.4	50	6	I29660	Sequence	164	13.2	37.7	28	6	I59697	I59697 Sequence
C	92	13.8	39.4	50	6	I91334	Sequence	165	13.2	37.7	28	6	I59703	I59703 Sequence
C	93	13.8	39.4	51	6	AX157821	Sequence	166	13.2	37.7	33	6	I11713	I11713 Sequence
C	94	13.8	39.4	51	6	AX159285	Sequence	167	13.2	37.7	41	6	AR002417	AR002417 Sequence
C	95	13.8	39.4	51	6	AX203685	Sequence	168	13.2	37.7	41	6	AR034607	AR034607 Sequence
C	96	13.8	39.4	59	6	AX011351	Sequence	169	13.2	37.7	41	6	I66285	I66285 Sequence
C	97	13.8	39.4	69	6	AF189384	Homo sapi	170	13.2	37.7	42	6	I79897	I79897 Sequence
C	98	13.8	39.4	81	6	I19318	Sequence	171	13.2	37.7	42	10	I08595	I08595 Sequence
C	99	13.8	39.4	81	14	AB001394	Hepatitis	172	13.2	37.7	42	10	MUSIDJCK	I36798 Mus muscullu
C	100	13.8	39.4	81	14	AB001396	Hepatitis	173	13.2	37.7	45	6	I11712	I11712 Sequence
C	101	13.8	39.4	81	14	AF207432	Hepatitis	174	13.2	37.7	50	6	AR032967	AR032967 Sequence
C	102	13.8	39.4	96	6	AX354334	Sequence	175	13.2	37.7	50	6	AR032968	AR032968 Sequence
C	103	13.8	39.4	100	6	AR142893	Sequence	176	13.2	37.7	50	6	I29707	I29707 Sequence
C	104	13.6	38.9	31	6	AR112220	Sequence	177	13.2	37.7	50	6	I29708	I29708 Sequence
C	105	13.6	38.9	31	6	AR112222	Sequence	178	13.2	37.7	50	6	I91381	I91381 Sequence
C	106	13.6	38.9	31	6	AR149262	Sequence	179	13.2	37.7	50	6	I91382	I91382 Sequence
C	107	13.6	38.9	31	6	AR149264	Sequence	180	13.2	37.7	51	6	AF189252	AF189252 Porcine
C	108	13.6	38.9	32	6	I26213	Sequence	181	13.2	37.7	51	6	A46976	A46976 Sequence
C	109	13.6	38.9	40	6	AR148771	Sequence	182	13.2	37.7	51	6	AR102344	AR102344 Sequence
C	110	13.6	38.9	42	6	AR100954	Sequence	183	13.2	37.7	51	6	AX141064	AX141064 Sequence
C	111	13.6	38.9	51	6	AX155976	Sequence	184	13.2	37.7	51	6	AX145934	AX145934 Sequence
C	112	13.6	38.9	51	6	AX162402	Sequence	185	13.2	37.7	51	6	AX159869	AX159869 Sequence
C	113	13.6	38.9	61	6	AR165812	Sequence	186	13.2	37.7	51	6	AX161095	AX161095 Sequence
C	114	13.6	38.9	72	11	G70637	Sequence	187	13.2	37.7	51	6	AX161097	AX161097 Sequence
C	115	13.6	38.9	76	14	FLAHAE	Sequence	188	13.2	37.7	54	6	AR165559	AR165559 Sequence
C	116	13.6	38.9	81	9	HSRCL233	Influenza v	189	13.2	37.7	54	6	AR022588	AR022588 Sequence
C	117	13.6	38.9	81	9	S80450	H.sapiens	190	13.2	37.7	54	6	AR037603	AR037603 Sequence
C	118	13.6	38.9	87	3	SUPHISAAF	S80450 V Delta 23-C	191	13.2	37.7	54	6	AR178061	AR178061 Sequence
C	119	13.6	38.9	89	6	AR2518	M25170 Sea urchin	192	13.2	37.7	57	6	HO1086S07	HO1086S07 Sequence
C	120	13.6	38.9	91	9	HSBCL228	AR2518 H.sapiens	193	13.2	37.7	60	6	E64748	E64748 Reagent for
C	121	13.6	38.9	93	9	AF417181	AF417181 Macaca mu	194	13.2	37.7	61	1	AF209514	AF209514 Escherich
C	122	13.4	38.3	28	6	AR159831	Sequence	195	13.2	37.7	62	6	AR040780	AR040780 Sequence
C	123	13.4	38.3	31	6	AX248432	Sequence	196	13.2	37.7	69	5	RRN28D8	RRN28D8 Sequence
C	124	13.4	38.3	32	6	AX174814	Sequence	197	13.2	37.7	72	5	RRN28D8	RRN28D8 Sequence
C	125	13.4	38.3	33	6	E51297	AX174814 Sequence	198	13.2	37.7	78	10	MWCA2IV7	MWCA2IV7 Sequence
C	126	13.4	38.3	33	6	E51118	E51297 Novel G pro	199	13.2	37.7	78	10	MUSMTTAA	MUSMTTAA Sequence
C	127	13.4	38.3	50	6	AX199480	E51118 Novel G pro	200	13.2	37.7	79	6	AR062564	AR062564 Sequence
C	128	13.4	38.3	50	6	AX199482	AX199480 Sequence	201	13.2	37.7	79	6	AR125968	AR125968 Sequence
C	129	13.4	38.3	50	6	AX199484	Sequence	202	13.2	37.7	79	6	I47288	I47288 Sequence
C	130	13.4	38.3	50	6	AX287016	Sequence	203	13.2	37.7	80	4	BTFTTIS1	BTFTTIS1 Sequence
C	131	13.4	38.3	51	6	AX159052	Sequence	204	13.2	37.7	84	6	AR002356	AR002356 Sequence
C	132	13.4	38.3	51	6	AX159409	Sequence	205	13.2	37.7	84	6	AR002385	AR002385 Sequence
C	133	13.4	38.3	51	6	AX1919185	Sequence	206	13.2	37.7	84	6	AR030859	AR030859 Sequence
C	134	13.4	38.3	51	6	AR254563	Sequence	207	13.2	37.7	84	6	AR030888	AR030888 Sequence
C	135	13.4	38.3	54	6	E54538	AF254563 Homo sapi	208	13.2	37.7	84	6	AR068254	AR068254 Sequence
C	136	13.4	38.3	55	6	A75807	E54538 Herpesvirus	209	13.2	37.7	84	6	AR068283	AR068283 Sequence
C	137	13.4	38.3	55	6	I73448	A75807 Sequence	210	13.2	37.7	84	6	I86805	I86805 Sequence
C	138	13.4	38.3	56	6	AX183555	I73448 Sequence	211	13.2	37.7	84	6	I86834	I86834 Sequence
C	139	13.4	38.3	56	6	HSADSDS07	AX183555 Sequence	212	13.2	37.7	84	6	AB0048534	AB0048534 Sequence
C	140	13.4	38.3	60	6	AX027956	AF000087 Homo sapi	213	13.2	37.7	85	10	MMCFYIN76	MMCFYIN76 Sequence
C	141	13.4	38.3	60	12	AX028053	AX027956 Sequence	214	13.2	37.7	86	6	E00062	E00062 DNA coding
C	142	13.4	38.3	69	6	AX287987	AX028053 Sequence	215	13.2	37.7	86	6	I02342	I02342 Sequence
C	143	13.4	38.3	69	6	AX287988	AX287987 Sequence	216	13.2	37.7	86	6	I07827	I07827 Sequence
C	144	13.4	38.3	75	9	HDMTF12	AX287988 Sequence	217	13.2	37.7	87	6	AR026137	AR026137 Sequence
C	145	13.4	38.3	78	3	AX013985	M13372 Human trans	218	13.2	37.7	90	1	VSHEMONT	X17305 Vltreoscll
C	146	13.4	38.3	79	9	HSRONP003	AX013985 Halichond	219	13.2	37.7	90	6	AX039250	AX039250 Sequence
							AF164635 Homo sapi						AX039490	AX039490 Sequence

C 220	13.2	37.7	90	6	AX134848	AX134848 Sequence	293	13	37.1	94	8	BUV35419	U35419 Beauveria v
C 221	13.2	37.7	90	6	AX134937	AX134937 Sequence	294	13	37.1	96	10	RNU78114	U78114 Rattus norv
C 222	13.2	37.7	90	6	AX135056	AX135056 Sequence	295	13	37.1	98	6	I08888	I08888 Sequence 6
C 223	13.2	37.7	99	9	HUMCG3A02	M10797 Human alpha	C 296	13	37.1	99	14	HIVFTRLH	M62311 Human immun
C 224	13	37.1	27	6	AX174820	AX174820 Sequence	C 297	13	37.1	100	9	AR18154	AJ008154 Homo sapi
C 225	13	37.1	29	6	AX343234	AX343234 Sequence	C 298	12.8	36.6	20	6	AR124970	AR124970 Sequence
C 226	13	37.1	29	6	AX353882	AX353882 Sequence	C 299	12.8	36.6	22	6	AR103422	AR103422 Sequence
C 227	13	37.1	30	6	AX148791	AX148791 Sequence	C 300	12.8	36.6	22	6	AR151630	AR151630 Sequence
C 228	13	37.1	30	6	AX148795	AX148795 Sequence	C 301	12.8	36.6	23	6	AR112025	AR112025 Sequence
C 229	13	37.1	32	6	AX280959	AX280959 Sequence	C 302	12.8	36.6	24	6	AM6988	AM6988 Sequence 28
C 230	13	37.1	33	9	HSAMW6B	X12101 H. sapiens (C 303	12.8	36.6	24	6	AR102351	AR102351 Sequence
C 231	13	37.1	36	6	AR003789	AR003789 Sequence	C 304	12.8	36.6	24	6	AX291070	AX291070 Sequence
C 232	13	37.1	36	6	AR010125	AR010125 Sequence	C 305	12.8	36.6	25	6	AR089449	AR089449 Sequence
C 233	13	37.1	36	6	AR055331	AR055331 Sequence	C 306	12.8	36.6	25	6	EA1384	EA1384 Amino acid
C 234	13	37.1	36	6	AR141260	AR141260 Sequence	C 307	12.8	36.6	26	6	AX043858	AX043858 Sequence
C 235	13	37.1	36	6	AR141497	AR141497 Sequence	C 308	12.8	36.6	28	6	AR091051	AR091051 Sequence
C 236	13	37.1	36	6	111971	111971 Sequence 83	C 309	12.8	36.6	31	6	144031	144031 Sequence 5
C 237	13	37.1	36	6	140542	140542 Sequence 81	C 310	12.8	36.6	39	6	AR116097	AR116097 Sequence
C 238	13	37.1	37	6	126193	126193 Sequence 26	C 311	12.8	36.6	39	6	145596	145596 Sequence 9
C 239	13	37.1	41	6	AR009877	AR009877 Sequence	C 312	12.8	36.6	40	6	115380	115380 Sequence 2
C 240	13	37.1	45	6	AX214211	AX214211 Sequence	C 313	12.8	36.6	42	6	AR038910	AR038910 Sequence
C 241	13	37.1	45	6	A05126	A05126 Oligonucleo	C 314	12.8	36.6	43	6	134859	134859 Sequence 2
C 242	13	37.1	46	6	AX214194	AX214194 Sequence	C 315	12.8	36.6	45	6	AX082539	AX082539 Sequence
C 243	13	37.1	46	6	AX214196	AX214196 Sequence	C 316	12.8	36.6	45	6	AX239597	AX239597 Sequence
C 244	13	37.1	46	6	AX214197	AX214197 Sequence	C 317	12.8	36.6	48	6	AX284152	AX284152 Sequence
C 245	13	37.1	46	6	AX214198	AX214198 Sequence	C 318	12.8	36.6	48	10	MUSTIGHVS	M22389 Mouse Ig ge
C 246	13	37.1	46	6	AX214200	AX214200 Sequence	C 319	12.8	36.6	50	9	HUMTCCV14	L39471 Homo sapien
C 247	13	37.1	46	6	AX214202	AX214202 Sequence	C 320	12.8	36.6	51	6	AX156887	AX156887 Sequence
C 248	13	37.1	46	6	AX214210	AX214210 Sequence	C 321	12.8	36.6	51	6	AX157569	AX157569 Sequence
C 249	13	37.1	48	6	AR024318	AR024318 Sequence	C 322	12.8	36.6	51	6	AX158218	AX158218 Sequence
C 250	13	37.1	48	6	AR035498	AR035498 Sequence	C 323	12.8	36.6	51	6	AX160961	AX160961 Sequence
C 251	13	37.1	48	6	AR045171	AR045171 Sequence	C 324	12.8	36.6	51	6	AX161093	AX161093 Sequence
C 252	13	37.1	48	6	BD011395	BD011395 Chimeric	C 325	12.8	36.6	51	6	AX161094	AX161094 Sequence
C 253	13	37.1	48	6	E43865	E43865 Chimeric an	C 326	12.8	36.6	51	6	AX161270	AX161270 Sequence
C 254	13	37.1	48	6	159449	159449 Sequence 7	C 327	12.8	36.6	51	6	AX161858	AX161858 Sequence
C 255	13	37.1	48	23	E11162	E11162 Oligonucleo	C 328	12.8	36.6	51	6	AX162652	AX162652 Sequence
C 256	13	37.1	50	6	AX190303	AX190303 Sequence	C 329	12.8	36.6	51	6	AX165327	AX165327 Sequence
C 257	13	37.1	50	8	AF302100S2	AF302099 Zea mays	C 330	12.8	36.6	51	6	AX190302	AX190302 Sequence
C 258	13	37.1	51	6	AX157215	AX157215 Sequence	C 331	12.8	36.6	51	6	AX199170	AX199170 Sequence
C 259	13	37.1	51	6	AX158869	AX158869 Sequence	C 332	12.8	36.6	51	6	AX204135	AX204135 Sequence
C 260	13	37.1	51	6	AX158871	AX158871 Sequence	C 333	12.8	36.6	51	6	AX141066	AX141066 Sequence
C 261	13	37.1	51	6	AX158873	AX158873 Sequence	C 334	12.8	36.6	54	6	AX146936	AX146936 Sequence
C 262	13	37.1	51	6	AX158874	AX158874 Sequence	C 335	12.8	36.6	59	9	AB010680	AB010680 Homo sapi
C 263	13	37.1	51	6	AX162070	AX162070 Sequence	C 336	12.8	36.6	60	6	A93059	A93059 Sequence 36
C 264	13	37.1	54	6	A38936	A38936 Sequence 23	C 337	12.8	36.6	60	6	AR009394	AR009394 Sequence
C 265	13	37.1	54	6	AR054332	AR054332 Sequence	C 338	12.8	36.6	60	6	AR098102	AR098102 Sequence
C 266	13	37.1	55	6	A58781	A58781 Sequence 27	C 339	12.8	36.6	60	6	E40779	E40779 Antihuman F
C 267	13	37.1	56	6	I23354	I23354 Sequence 8	C 340	12.8	36.6	60	6	E65258	E65258 Mutant of E
C 268	13	37.1	60	6	AR051733	AR051733 Sequence	C 341	12.8	36.6	65	9	AB032807	AB032807 Homo sapi
C 269	13	37.1	60	6	AR173991	AR173991 Sequence	C 342	12.8	36.6	66	5	CHKC1A212	J00837 Chicken alp
C 270	13	37.1	64	12	SYNECCOYO	M18153 E.coli synt	C 343	12.8	36.6	66	11	HSU84997	U84997 Homo sapien
C 271	13	37.1	66	6	AX288022	AX288022 Sequence	C 344	12.8	36.6	68	1	ECFXMNTG	X05336 E.coli DNA
C 272	13	37.1	70	11	HUMSMX666	L24887 Human Chrom	C 345	12.8	36.6	69	1	RC23SMB16	Y09736 R.galgae 2
C 273	13	37.1	71	6	I23355	I23355 Sequence 9	C 346	12.8	36.6	70	10	MMVIMV60	X89177 M.musculus
C 274	13	37.1	72	6	AR140803	AR140803 Sequence	C 347	12.8	36.6	71	5	LRN28D8	Z18735 Limanda 11m
C 275	13	37.1	72	6	AX150235	AX150235 Sequence	C 348	12.8	36.6	71	6	A82520	AB2520 Sequence 23
C 276	13	37.1	72	6	193482	193482 Sequence 80	C 349	12.8	36.6	71	6	AR054780	AR054780 Sequence
C 277	13	37.1	72	6	195109	195109 Sequence 80	C 350	12.8	36.6	71	6	AR066045	AR066045 Sequence
C 278	13	37.1	73	5	SCRN28D8	Z18748 Scylliorhinu	C 351	12.8	36.6	74	9	H010868512	AR21397 Homo sapi
C 279	13	37.1	73	6	AR017753	AR017753 Sequence	C 352	12.8	36.6	78	5	S67414	S67414 [short lntle
C 280	13	37.1	73	6	AR094930	AR094930 Sequence	C 353	12.8	36.6	78	5	AX336617	AX336617 Sequence
C 281	13	37.1	73	6	AR165589	AR165589 Sequence	C 354	12.8	36.6	79	6	I04423	I04423 Sequence 21
C 282	13	37.1	73	9	HUMMACAB	L37714 Homo sapien	C 355	12.8	36.6	79	6	I04459	I04459 Sequence 57
C 283	13	37.1	78	10	MUSMTMFAA	M36651 Mouse mitoc	C 356	12.8	36.6	84	6	AR018996	AR018996 Sequence
C 284	13	37.1	81	6	AR127695	AR127695 Sequence	C 357	12.8	36.6	84	6	AR037739	AR037739 Sequence
C 285	13	37.1	81	6	175364	175364 Sequence 11	C 358	12.8	36.6	84	6	133747	I33747 Sequence 43
C 286	13	37.1	81	9	AF267839	AF267839 Homo sapi	C 359	12.8	36.6	84	6	134686	I34686 Sequence 43
C 287	13	37.1	87	6	AR111211	AR111211 Sequence	C 360	12.8	36.6	89	5	CHKCOLA12	M25967 Chicken alp
C 288	13	37.1	89	6	AX317792	AX317792 Sequence	C 361	12.8	36.6	90	10	MUSTGAPCJ	M32004 Mus musculu
C 289	13	37.1	92	9	HSPA24H1	Z79166 H.sapiens f	C 362	12.8	36.6	94	11	AF049032	AF049032 Homo sapi
C 290	13	37.1	93	9	HS186XD2	Z17252 H.sapiens f	C 363	12.8	36.6	94	11	AF049030	AF049030 Homo sapi
C 291	13	37.1	94	6	AR165706	AR165706 Sequence	C 364	12.8	36.6	99	6	AR094319	AR094319 Sequence
C 292	13	37.1	94	8	AV288SD1	Z54119 A.virelium	C 365	12.8	36.6	100	14	S6786651	S67866 gag-p24...e

C 366	12.6	36.0	20	6	A46375	Sequence 12	439	12.6	36.0	80	6	AR042781	AR042781 Sequence
C 367	12.6	36.0	20	6	AR027714	Sequence	440	12.6	36.0	81	14	AB001391	AB001391 Hepatitis
C 368	12.6	36.0	20	6	AR170525	Sequence	441	12.6	36.0	81	14	AB001395	AB001395 Hepatitis
C 369	12.6	36.0	21	6	AX356189	Sequence	442	12.6	36.0	82	3	BRAH0X3G	L14883 Branchiost
C 370	12.6	36.0	24	6	AX292404	Sequence	443	12.6	36.0	86	5	S76800	S76800 anion excha
C 371	12.6	36.0	24	6	E59935	Human male-	444	12.6	36.0	94	8	AF372982	AF372982 Pneumocys
C 372	12.6	36.0	27	6	AX116972	Sequence	445	12.6	36.0	96	14	HIVLRID	M62307 Human Immun
C 373	12.6	36.0	28	6	AR097136	Sequence	446	12.6	36.0	96	14	HIVLRID	M62308 Human Immun
C 374	12.6	36.0	28	6	AR130634	Sequence	447	12.6	36.0	97	8	AF372984	AF372984 Pneumocys
C 375	12.6	36.0	28	6	AR171983	Sequence	448	12.6	36.0	98	6	I35455	I35455 Sequence 6
C 376	12.6	36.0	30	6	A62195	Sequence 89	449	12.6	36.0	100	6	AR097087	AR097087 Sequence
C 377	12.6	36.0	30	6	A62202	Sequence 96	450	12.6	36.0	100	6	AR130585	AR130585 Sequence
C 378	12.6	36.0	30	6	AX022419	Sequence	451	12.6	36.0	100	6	AR142893	AR142893 Sequence
C 379	12.6	36.0	30	6	AX022426	Sequence	452	12.6	36.0	100	6	AR142895	AR142895 Sequence
C 380	12.6	36.0	31	6	I37086	Sequence 99	453	12.6	36.0	100	6	AR142897	AR142897 Sequence
C 381	12.6	36.0	31	6	I37087	Sequence 10	454	12.6	36.0	100	6	AR171934	AR171934 Sequence
C 382	12.6	36.0	31	6	I93936	Sequence 99	455	12.6	36.0	100	6	AX020206	AX020206 Sequence
C 383	12.6	36.0	31	6	I93937	Sequence 10	456	12.4	35.4	17	6	AX139142	AX139142 Sequence
C 384	12.6	36.0	36	6	AR040920	Sequence	457	12.4	35.4	18	6	AX193594	AX193594 Sequence
C 385	12.6	36.0	36	6	AR051827	Sequence	458	12.4	35.4	21	6	AR078239	AR078239 Sequence
C 386	12.6	36.0	36	6	AR151563	Sequence	459	12.4	35.4	21	6	AR168136	AR168136 Sequence
C 387	12.6	36.0	36	6	AR127330	Sequence	460	12.4	35.4	21	6	AX133294	AX133294 Sequence
C 388	12.6	36.0	36	6	AR148975	Sequence	461	12.4	35.4	21	6	E15432	E15432 Linker. 7/1
C 389	12.6	36.0	36	6	AR168644	Sequence	462	12.4	35.4	21	6	E15437	E15437 Linker. 7/1
C 390	12.6	36.0	36	6	AR170227	Sequence	463	12.4	35.4	24	6	A13726	A13726 Oligonucleot
C 391	12.6	36.0	36	6	AR171666	Sequence	464	12.4	35.4	24	6	A13729	A13729 Oligonucleot
C 392	12.6	36.0	36	6	AX016752	Sequence	465	12.4	35.4	24	6	AR084223	AR084223 Sequence
C 393	12.6	36.0	36	6	AX016769	Sequence	466	12.4	35.4	24	6	I90366	I90366 Sequence 10
C 394	12.6	36.0	36	6	BD011556	DNA mutag	467	12.4	35.4	25	6	AR078240	AR078240 Sequence
C 395	12.6	36.0	36	6	I36217	Sequence 19	468	12.4	35.4	25	6	E15433	E15433 Linker. 7/1
C 396	12.6	36.0	38	6	I74673	Sequence 2	469	12.4	35.4	25	6	E15438	E15438 Linker. 7/1
C 397	12.6	36.0	38	6	I91759	Sequence 2	470	12.4	35.4	27	6	AR060293	AR060293 Sequence
C 398	12.6	36.0	41	6	AR174282	Sequence	471	12.4	35.4	27	6	AX138047	AX138047 Sequence
C 399	12.6	36.0	41	6	AX074208	Sequence	472	12.4	35.4	27	6	E31816	E31816 Method for
C 400	12.6	36.0	41	6	AX074210	Sequence	473	12.4	35.4	27	6	I20953	I20953 Sequence 20
C 401	12.6	36.0	41	6	AX299784	Sequence	474	12.4	35.4	30	6	AR160339	AR160339 Sequence
C 402	12.6	36.0	41	6	AX327075	Sequence	475	12.4	35.4	30	6	E27464	E27464 Novel gene
C 403	12.6	36.0	41	6	AX327076	Sequence	476	12.4	35.4	31	6	A06219	A06219 Synthetic D
C 404	12.6	36.0	42	5	CHKC1A218	Sequence	477	12.4	35.4	31	6	AX249023	AX249023 Sequence
C 405	12.6	36.0	44	23	E10886	Sequence	478	12.4	35.4	31	6	AX249041	AX249041 Sequence
C 406	12.6	36.0	47	6	AR125794	Sequence	479	12.4	35.4	33	6	AR044275	AR044275 Sequence
C 407	12.6	36.0	47	6	AX194784	Sequence	480	12.4	35.4	33	6	I35915	I35915 Sequence 15
C 408	12.6	36.0	47	6	AX195033	Sequence	481	12.4	35.4	33	6	I68888	I68888 Sequence 15
C 409	12.6	36.0	47	6	I47206	Sequence 13	482	12.4	35.4	34	6	BD010130	BD010130 Peptide 1
C 410	12.6	36.0	49	6	AX209945	Sequence	483	12.4	35.4	35	6	AX052699	AX052699 Sequence
C 411	12.6	36.0	50	9	D87876	Human DNA f	484	12.4	35.4	37	6	BD010144	BD010144 Peptide 1
C 412	12.6	36.0	51	6	AX115657	Sequence	485	12.4	35.4	38	6	E13570	E13570 prG3 primer
C 413	12.6	36.0	51	6	AX158248	Sequence	486	12.4	35.4	42	6	AR063149	AR063149 Sequence
C 414	12.6	36.0	51	6	AX158248	Sequence	487	12.4	35.4	42	6	AR146454	AR146454 Sequence
C 415	12.6	36.0	51	6	AX158630	Sequence	488	12.4	35.4	42	10	MNTCRBBS	X80370 M. musculus
C 416	12.6	36.0	51	6	AX160620	Sequence	489	12.4	35.4	45	6	AR044896	AR044896 Sequence
C 417	12.6	36.0	51	6	AX161776	Sequence	490	12.4	35.4	45	6	AX054985	AX054985 Sequence
C 418	12.6	36.0	51	6	AX162679	Sequence	491	12.4	35.4	45	6	I34761	I34761 Sequence 5
C 419	12.6	36.0	51	6	AX164995	Sequence	492	12.4	35.4	45	6	I54985	I54985 Sequence 5
C 420	12.6	36.0	51	6	AX190169	Sequence	493	12.4	35.4	45	6	I55005	I55005 Sequence 29
C 421	12.6	36.0	51	6	AX199083	Sequence	494	12.4	35.4	45	9	H0MTGRABH	L06994 Human 19 re
C 422	12.6	36.0	51	6	AX199266	Sequence	495	12.4	35.4	45	9	S80699	S80699 gamma delta
C 423	12.6	36.0	51	6	AX327739	Sequence	496	12.4	35.4	47	6	A51629	A51629 Sequence 39
C 424	12.6	36.0	51	6	AX327814	Sequence	497	12.4	35.4	47	6	AX211584	AX211584 Sequence
C 425	12.6	36.0	54	6	AX338572	Sequence	498	12.4	35.4	48	6	AX201575	AX201575 Sequence
C 426	12.6	36.0	54	10	AX299787	Sequence	499	12.4	35.4	48	6	E40044	E40044 Drug contai
C 427	12.6	36.0	60	6	A29431	Mus muscu	500	12.4	35.4	48	6	E40852	E40852 Humanized a
C 428	12.6	36.0	60	6	D86103	Sequence ex	501	12.4	35.4	48	6	E43398	E43398 Humanized a
C 429	12.6	36.0	61	6	AR165797	Sequence	502	12.4	35.4	49	6	AR050693	AR050693 Sequence
C 430	12.6	36.0	71	6	AR140784	Sequence	503	12.4	35.4	49	14	BCL2A	M10859 Ia Crose b
C 431	12.6	36.0	71	6	I08218	Sequence 12	504	12.4	35.4	50	6	AR063148	AR063148 Sequence
C 432	12.6	36.0	71	6	I93463	Sequence 61	505	12.4	35.4	50	6	AR146453	AR146453 Sequence
C 433	12.6	36.0	71	6	I95090	Sequence 61	506	12.4	35.4	50	6	AX119911	AX119911 Sequence
C 434	12.6	36.0	74	6	E00316	Probe of IG	507	12.4	35.4	51	6	AX157174	AX157174 Sequence
C 435	12.6	36.0	74	6	I04048	Sequence 2	508	12.4	35.4	51	6	AX157418	AX157418 Sequence
C 436	12.6	36.0	76	9	HS298231	Sequence	509	12.4	35.4	51	6	AX157703	AX157703 Sequence
C 437	12.6	36.0	77	8	HS298231	Physconia	510	12.4	35.4	51	6	AX157704	AX157704 Sequence
C 438	12.6	36.0	80	6	AR042770	Sequence	511	12.4	35.4	51	6	AX158027	AX158027 Sequence

C 512	12.4	35.4	51	6	AX199437	Sequence	585	12.4	35.4	90	9	D50749	D50749 Human mRNA
C 513	12.4	35.4	51	9	HSTRREC	X69178 H.sapiens m	586	12.4	35.4	90	9	HUMHTRV109	D32022 Human mRNA
C 514	12.4	35.4	52	6	AX025599	AX025599 Sequence	C 587	12.4	35.4	90	9	AF267761	D2267761 Homo sapi
C 515	12.4	35.4	54	6	E04548	E04548 DNA contain	C 588	12.4	35.4	91	6	A82523	A82523 Sequence 26
C 516	12.4	35.4	55	6	A32052	A32052 DNA probe (C 589	12.4	35.4	91	6	A82523	A82523 Sequence 26
C 517	12.4	35.4	55	6	A32071	A32071 DNA probe (C 590	12.4	35.4	94	9	HSIGD2110	X33614 H.sapiens g
C 518	12.4	35.4	56	23	E10872	E10872 PCR primer	C 591	12.4	35.4	96	6	I08951	I08951 Sequence 17
C 519	12.4	35.4	58	6	A02573	A02573 Nucleotide	C 592	12.4	35.4	96	6	AB044130	AB044130 Homo sapi
C 520	12.4	35.4	58	6	A49961	A49961 Sequence 21	C 593	12.4	35.4	97	6	AX326639	AX326639 Sequence
C 521	12.4	35.4	59	9	S49040	S49040 Immunoglobul	C 594	12.4	35.4	97	6	AX326672	AX326672 Sequence
C 522	12.4	35.4	60	6	I08965	I08965 Sequence 41	C 595	12.4	34.9	17	6	AX226764	AX226764 Sequence
C 523	12.4	35.4	60	10	MUSGAGAB	M38072 Mouse circ	C 596	12.2	34.9	20	6	AR100391	AR100391 Sequence
C 524	12.4	35.4	62	6	AX083959	AX083959 Sequence	C 597	12.2	34.9	20	6	AR150046	AR150046 Sequence
C 525	12.4	35.4	64	6	AR002986	AR002986 Sequence	C 598	12.2	34.9	20	6	AX033008	AX033008 Sequence
C 526	12.4	35.4	64	6	AR002987	AR002987 Sequence	C 599	12.2	34.9	20	6	AX195875	AX195875 Sequence
C 527	12.4	35.4	64	9	HUMMT450A	L31679 Human STS U	C 600	12.2	34.9	20	6	E14347	E14347 Primer. 7/1
C 528	12.4	35.4	66	6	A42858	A42858 Sequence 12	C 601	12.2	34.9	22	6	AX068228	AX068228 Sequence
C 529	12.4	35.4	66	6	A49963	A49963 Sequence 23	C 602	12.2	34.9	22	6	AX077187	AX077187 Sequence
C 530	12.4	35.4	66	6	AR065667	AR065667 Sequence	C 603	12.2	34.9	23	6	E35223	E35223 Human monoc
C 531	12.4	35.4	66	6	AR146036	AR146036 Sequence	C 604	12.2	34.9	23	6	E37610	E37610 Monoclonal
C 532	12.4	35.4	67	6	A38557	A38557 Sequence 17	C 605	12.2	34.9	25	6	A15104	A15104 Oligonucleo
C 533	12.4	35.4	68	6	A41482	A41482 Sequence 8	C 606	12.2	34.9	25	6	A26157	A26157 Synthetic o
C 534	12.4	35.4	69	3	DRORGMAS1	K01579 d.melanog	C 607	12.2	34.9	25	6	AX096347	AX096347 Sequence
C 535	12.4	35.4	69	6	A41479	A41479 Sequence 5	C 608	12.2	34.9	26	6	AR049821	AR049821 Sequence
C 536	12.4	35.4	69	9	S59798514	S59813 PKLR-L-type	C 609	12.2	34.9	26	6	AR080210	AR080210 Sequence
C 537	12.4	35.4	69	23	E11404	E11404 Linker. 9/2	C 610	12.2	34.9	26	6	AR149715	AR149715 Sequence
C 538	12.4	35.4	72	6	I03057	I03057 Sequence 4	C 611	12.2	34.9	26	6	AX037965	AX037965 Sequence
C 539	12.4	35.4	72	6	I03718	I03718 Sequence 9	C 612	12.2	34.9	27	6	AR143836	AR143836 Sequence
C 540	12.4	35.4	73	1	CLTSTRRB	M4685 Calliothrix	C 613	12.2	34.9	27	6	AX305040	AX305040 Sequence
C 541	12.4	35.4	75	6	A49912	A49912 Sequence 4	C 614	12.2	34.9	27	6	I06147	I06147 Sequence 4
C 542	12.4	35.4	75	6	A49942	A49942 Sequence 2	C 615	12.2	34.9	29	6	AX236821	AX236821 Sequence
C 543	12.4	35.4	76	6	A49941	A49941 Sequence 1	C 616	12.2	34.9	30	6	A82564	A82564 Sequence 38
C 544	12.4	35.4	76	9	S63975	S63975 IGH (CDR3 r	C 617	12.2	34.9	30	6	AR162012	AR162012 Sequence
C 545	12.4	35.4	77	6	A38560	A38560 Sequence 20	C 618	12.2	34.9	30	6	AX148783	AX148783 Sequence
C 546	12.4	35.4	78	10	AF020740	AF020740 Mus muscu	C 619	12.2	34.9	30	6	I06520	I06520 Sequence 24
C 547	12.4	35.4	78	10	S639455	S69227 p53 (Intlon	C 620	12.2	34.9	31	6	AX249417	AX249417 Sequence
C 548	12.4	35.4	80	6	AX002557	AX002557 Sequence	C 621	12.2	34.9	32	6	AX141256	AX141256 Sequence
C 549	12.4	35.4	80	6	E27445	E27445 cdc25B Gene	C 622	12.2	34.9	34	6	AX016728	AX016728 Sequence
C 550	12.4	35.4	80	11	HUMSWS11	L24816 Human chrom	C 623	12.2	34.9	34	6	E40006	E40006 Drug contai
C 551	12.4	35.4	80	14	AF040807	AF040807 Hepatitis	C 624	12.2	34.9	34	6	E40814	E40814 Humanized a
C 552	12.4	35.4	81	6	AR101957	AR101957 Sequence	C 625	12.2	34.9	34	6	E43360	E43360 Humanized a
C 553	12.4	35.4	81	6	AR177447	AR177447 Sequence	C 626	12.2	34.9	36	6	A04715	A04715 Nucleotide
C 554	12.4	35.4	81	14	AF040801	AF040801 Hepatitis	C 627	12.2	34.9	36	6	A04715	A04715 Nucleotide
C 555	12.4	35.4	81	14	AF040803	AF040803 Hepatitis	C 628	12.2	34.9	36	6	A04723	A04723 Nucleotide
C 556	12.4	35.4	81	14	AF040806	AF040806 Hepatitis	C 629	12.2	34.9	36	6	A04749	A04749 reverse com
C 557	12.4	35.4	81	14	AF207208	AF207208 Hepatitis	C 630	12.2	34.9	36	6	A17657	A17657 Nucleotide
C 558	12.4	35.4	82	3	DRORGM21V	K01282 D.villitis 2	C 631	12.2	34.9	36	6	AR138465	AR138465 Sequence
C 559	12.4	35.4	82	6	A16191	A16191 multiple cl	C 632	12.2	34.9	36	6	AR138466	AR138466 Sequence
C 560	12.4	35.4	82	6	A16192	A16192 multiple cl	C 633	12.2	34.9	36	6	AX088153	AX088153 Sequence
C 561	12.4	35.4	82	6	A60536	A60536 Sequence 1	C 634	12.2	34.9	36	6	AX088154	AX088154 Sequence
C 562	12.4	35.4	82	6	A72353	A72353 Sequence 1	C 635	12.2	34.9	36	6	S81253	S81253 T cell anti
C 563	12.4	35.4	82	6	AX045648	AX045648 Sequence	C 636	12.2	34.9	38	6	A04718	A04718 Nucleotide
C 564	12.4	35.4	83	3	S65068	S59832 PKLR-L-type	C 637	12.2	34.9	38	6	A04718	A04718 Nucleotide
C 565	12.4	35.4	84	3	S65068	S55068 VDI/RPD al	C 638	12.2	34.9	38	6	A04722	A04722 Nucleotide
C 566	12.4	35.4	86	6	A64178	A64178 Sequence 44	C 639	12.2	34.9	38	6	A04748	A04748 Nucleotide
C 567	12.4	35.4	86	6	A68364	A68364 Sequence 44	C 640	12.2	34.9	38	6	A17656	A17656 Nucleotide
C 568	12.4	35.4	86	6	AR031287	AR031287 Sequence	C 641	12.2	34.9	40	6	A42979	A42979 Sequence 14
C 569	12.4	35.4	86	6	AR036409	AR036409 Sequence	C 642	12.2	34.9	40	6	A45525	A45525 Sequence 10
C 570	12.4	35.4	86	6	AR060841	AR060841 Sequence	C 643	12.2	34.9	40	6	AR030797	AR030797 Sequence
C 571	12.4	35.4	86	6	AR065996	AR065996 Sequence	C 644	12.2	34.9	40	6	AR082134	AR082134 Sequence
C 572	12.4	35.4	86	6	AR088950	AR088950 Sequence	C 645	12.2	34.9	40	6	E05618	E05618 Primer for
C 573	12.4	35.4	87	9	AB044126	AB044126 Homo sapi	C 646	12.2	34.9	41	6	AR034524	AR034524 Sequence
C 574	12.4	35.4	87	9	HSIGD217	X33615 H.sapiens g	C 647	12.2	34.9	41	6	AR048624	AR048624 Sequence
C 575	12.4	35.4	87	9	HSU5099	U55099 Human isola	C 648	12.2	34.9	42	6	AX107166	AX107166 Sequence
C 576	12.4	35.4	87	14	S5784652	S57847 Sigma virus	C 649	12.2	34.9	42	6	I44820	I44820 Sequence 44
C 577	12.4	35.4	88	9	HSIGD219	X33616 H.sapiens g	C 650	12.2	34.9	42	10	MUSTGDCJF	L36780 Mus musculu
C 578	12.4	35.4	88	9	HSIGD2212	X33617 H.sapiens g	C 651	12.2	34.9	43	6	E01929	E01929 Synthetic D
C 579	12.4	35.4	88	9	HSIGD237	X33618 H.sapiens g	C 652	12.2	34.9	43	6	E02301	E02301 DNA encodin
C 580	12.4	35.4	89	6	AR101956	AR101956 Sequence	C 653	12.2	34.9	46	6	AX107167	AX107167 Sequence
C 581	12.4	35.4	89	6	AR177446	AR177446 Sequence	C 654	12.2	34.9	47	6	AR080868	AR080868 Sequence
C 582	12.4	35.4	90	3	DME426729	A426729 Drosophila	C 655	12.2	34.9	48	6	A10302	A10302 pUR278 frag
C 583	12.4	35.4	90	6	I36128	I36128 Sequence 12	C 656	12.2	34.9	48	6	I05454	I05454 Sequence 6
C 584	12.4	35.4	90	9	AB044114	AB044114 Homo sapi	C 657	12.2	34.9	48	9	HSTCELL8	X81543 H.sapiens r

658	12.2	34.9	48	10	S60821	S60821 VH7183=immu	731	12.2	34.9	81	6	I19308	I19308 Sequence 80
659	12.2	34.9	48	14	S57687	S57687 coat protei	732	12.2	34.9	81	6	I19309	I19309 Sequence 81
660	12.2	34.9	49	6	E00628	E00628 Synthetic D	733	12.2	34.9	81	6	I24687	I24687 Sequence 14
661	12.2	34.9	49	23	E10516	E10516 DNA of a pa	734	12.2	34.9	81	14	AB001410	AB001410 Hepatitis
662	12.2	34.9	50	9	HUMSAU3A36	D49620 Human alphi	735	12.2	34.9	81	14	AF207402	AF207402 Hepatitis
663	12.2	34.9	50	9	HUMSAU3A64	D49648 Human alphi	736	12.2	34.9	81	14	AF207403	AF207403 Hepatitis
664	12.2	34.9	51	6	AX157822	AX157822 Sequence	737	12.2	34.9	81	14	AF207405	AF207405 Hepatitis
665	12.2	34.9	51	6	AX157859	AX157859 Sequence	738	12.2	34.9	81	14	AF207407	AF207407 Hepatitis
666	12.2	34.9	51	6	AX158332	AX158332 Sequence	739	12.2	34.9	81	14	AF207408	AF207408 Hepatitis
667	12.2	34.9	51	6	AX158604	AX158604 Sequence	740	12.2	34.9	81	14	AF207409	AF207409 Hepatitis
668	12.2	34.9	51	6	AX159837	AX159837 Sequence	741	12.2	34.9	81	14	AF207411	AF207411 Hepatitis
669	12.2	34.9	51	6	AX159838	AX159838 Sequence	742	12.2	34.9	81	14	AF207412	AF207412 Hepatitis
670	12.2	34.9	51	6	AX161455	AX161455 Sequence	743	12.2	34.9	81	14	AF207413	AF207413 Hepatitis
671	12.2	34.9	51	6	AX161663	AX161663 Sequence	744	12.2	34.9	81	14	AF207414	AF207414 Hepatitis
672	12.2	34.9	51	6	AX165590	AX165590 Sequence	745	12.2	34.9	81	14	AF207415	AF207415 Hepatitis
673	12.2	34.9	51	6	AX165681	AX165681 Sequence	746	12.2	34.9	81	14	AF207416	AF207416 Hepatitis
674	12.2	34.9	51	6	E37824	E37824 Human delta	747	12.2	34.9	81	14	AF207417	AF207417 Hepatitis
675	12.2	34.9	52	6	E41694	E41694 Process for	748	12.2	34.9	81	14	AF207418	AF207418 Hepatitis
676	12.2	34.9	53	9	AF082215	AF082215 Homo sapi	749	12.2	34.9	81	14	AF207420	AF207420 Hepatitis
677	12.2	34.9	57	6	BD010843	BD010843 HCV poly	750	12.2	34.9	81	14	AF207421	AF207421 Hepatitis
678	12.2	34.9	59	9	HUMSAU3A62	D49646 Human alphi	751	12.2	34.9	81	14	AF207422	AF207422 Hepatitis
679	12.2	34.9	59	12	SYNECOSD	M1485 E.coli deri	752	12.2	34.9	81	14	AF207423	AF207423 Hepatitis
680	12.2	34.9	60	6	A24685	A24685 primer 2228	753	12.2	34.9	81	14	AF207424	AF207424 Hepatitis
681	12.2	34.9	60	6	BD010845	BD010845 HCV poly	754	12.2	34.9	81	14	AF207425	AF207425 Hepatitis
682	12.2	34.9	60	6	E22195	E22195 Yeast capab	755	12.2	34.9	81	14	AF207428	AF207428 Hepatitis
683	12.2	34.9	60	6	S59796S01	S59796 PKLR=L-type	756	12.2	34.9	81	14	AF207429	AF207429 Hepatitis
684	12.2	34.9	61	6	AR171505	AR171505 Sequence	757	12.2	34.9	81	14	AF207430	AF207430 Hepatitis
685	12.2	34.9	61	6	BD005525	BD005525 Compositi	758	12.2	34.9	81	14	AF207433	AF207433 Hepatitis
686	12.2	34.9	61	10	MMVSI519X1	269835 M.musculus	759	12.2	34.9	81	14	AF207434	AF207434 Hepatitis
687	12.2	34.9	62	6	AR156363	AR156363 Sequence	760	12.2	34.9	81	14	AF207435	AF207435 Hepatitis
688	12.2	34.9	62	6	I19348	I19348 Sequence 19	761	12.2	34.9	81	14	AF207436	AF207436 Hepatitis
689	12.2	34.9	63	6	E03208	E03208 DNA encodin	762	12.2	34.9	81	14	AF207437	AF207437 Hepatitis
690	12.2	34.9	65	6	AR042688	AR042688 Sequence	763	12.2	34.9	81	14	AF207438	AF207438 Hepatitis
691	12.2	34.9	65	6	AR064821	AR064821 Sequence	764	12.2	34.9	81	14	AF207439	AF207439 Hepatitis
692	12.2	34.9	66	12	SYNRCFSYN	M61009 Synthetic E	765	12.2	34.9	81	14	AF207440	AF207440 Hepatitis
693	12.2	34.9	67	6	A26547	A26547 NH2-termina	766	12.2	34.9	81	14	AF207441	AF207441 Hepatitis
694	12.2	34.9	68	6	E01976	E01976 DNA encodin	767	12.2	34.9	81	14	AF207468	AF207468 Hepatitis
695	12.2	34.9	68	6	I21518	I21518 Sequence 65	768	12.2	34.9	81	14	AF207469	AF207469 Hepatitis
696	12.2	34.9	68	6	I21519	I21519 Sequence 66	769	12.2	34.9	81	14	AF207470	AF207470 Hepatitis
697	12.2	34.9	69	5	TM076077	U76077 Crypturellu	770	12.2	34.9	81	14	AF207471	AF207471 Hepatitis
698	12.2	34.9	69	9	MOKPN101	X01019 Monkey Kpni	771	12.2	34.9	81	14	AF207472	AF207472 Hepatitis
699	12.2	34.9	70	6	AR174779	AR174779 Sequence	772	12.2	34.9	81	14	AF207473	AF207473 Hepatitis
700	12.2	34.9	70	9	S69040	S69040 Homo sapien	773	12.2	34.9	81	14	AF207476	AF207476 Hepatitis
701	12.2	34.9	71	5	SPRN28D8	Z18761 Sardinia pil	774	12.2	34.9	81	14	AF207477	AF207477 Hepatitis
702	12.2	34.9	71	6	AR165767	AR165767 Sequence	775	12.2	34.9	81	14	AF207478	AF207478 Hepatitis
703	12.2	34.9	71	6	I13485	I13485 Sequence 19	776	12.2	34.9	81	14	AF207479	AF207479 Hepatitis
704	12.2	34.9	72	6	A32815	A32815 Synthetic p	777	12.2	34.9	81	14	AF207480	AF207480 Hepatitis
705	12.2	34.9	72	6	A32816	A32816 Synthetic p	778	12.2	34.9	81	6	AR005332	AR005332 Sequence
706	12.2	34.9	72	9	HSWCRBC1	X74391 H.sapiens (779	12.2	34.9	83	6	AR059860	AR059860 Sequence
707	12.2	34.9	72	9	AR189565	AR189565 Homo sapi	780	12.2	34.9	83	6	AR156117	AR156117 Sequence
708	12.2	34.9	72	10	S64321	S64321 VEGF188=vas	781	12.2	34.9	83	6	E03019	E03019 DNA encodin
709	12.2	34.9	73	6	AR012422	AR012422 Sequence	782	12.2	34.9	83	9	HSRNP2515	HSRNP2515
710	12.2	34.9	73	6	AR020250	AR020250 Sequence	783	12.2	34.9	83	11	AF275612	AF275612 Bos tauru
711	12.2	34.9	73	6	AR109271	AR109271 Sequence	784	12.2	34.9	85	6	AX047783	AX047783 Sequence
712	12.2	34.9	73	6	I82596	I82596 Sequence 37	785	12.2	34.9	85	6	E00061	E00061 DNA coding
713	12.2	34.9	73	7	S52492	S52492 [alpha sale	786	12.2	34.9	85	6	I02341	I02341 Sequence 2
714	12.2	34.9	73	23	E09522	E09522 Synthetic D	787	12.2	34.9	85	6	I07826	I07826 Sequence 2
715	12.2	34.9	74	6	AX233510	AX233510 Sequence	788	12.2	34.9	86	6	AX240926	AX240926 Sequence
716	12.2	34.9	74	6	AX233511	AX233511 Sequence	789	12.2	34.9	86	6	E03108	E03108 DNA encodin
717	12.2	34.9	74	6	I23998	I23998 Sequence 25	790	12.2	34.9	87	6	AX039235	AX039235 Sequence
718	12.2	34.9	75	5	OUTM9HC	OUTM958 Quail (C.co	791	12.2	34.9	87	6	AX039475	AX039475 Sequence
719	12.2	34.9	75	6	AR035204	AR035204 Sequence	792	12.2	34.9	87	6	AX134633	AX134633 Sequence
720	12.2	34.9	76	6	AF209175	AF209175 Homo sapi	793	12.2	34.9	87	6	AX134922	AX134922 Sequence
721	12.2	34.9	76	12	SYNLACLEX	M12203 E.coli lac	794	12.2	34.9	87	6	AX135041	AX135041 Sequence
722	12.2	34.9	77	6	E02812	E02812 DNA sequenc	795	12.2	34.9	87	6	I02343	I02343 Sequence 4
723	12.2	34.9	77	6	E02923	E02923 DNA sequenc	796	12.2	34.9	87	6	I07828	I07828 Sequence 4
724	12.2	34.9	77	6	E02927	E02927 DNA sequenc	797	12.2	34.9	87	12	SYND2H9	SYND2H9 Influenza A
725	12.2	34.9	77	6	E03005	E03005 DNA encodin	798	12.2	34.9	88	6	AR005324	AR005324 Sequence
726	12.2	34.9	77	6	I20794	I20794 Sequence 7	799	12.2	34.9	88	6	AR059852	AR059852 Sequence
727	12.2	34.9	77	6	I28743	I28743 Sequence 7	800	12.2	34.9	88	6	AR156109	AR156109 Sequence
728	12.2	34.9	77	6	I44748	I44748 Sequence 11	801	12.2	34.9	89	11	G64017	G64017 284Sp6 Huma
729	12.2	34.9	77	6	I44844	I44844 Sequence 11	802	12.2	34.9	90	4	BOVPRFA6	M1345 Bovine prep
730	12.2	34.9	77	6	I59528	I59528 Sequence 11	803	12.2	34.9	90	6	AX287819	AX287819 Sequence

C 804	12.2	34.9	90	9	S81328	S81328 IgJHC delta	C 877	12	34.3	33	6	AX280737	AX280737 Sequence
805	12.2	34.9	90	9	AF417179	AF417179 Macaca mu	878	12	34.3	33	6	AX280738	AX280738 Sequence
806	12.2	34.9	91	6	A10364	A10364 Nucleotide	879	12	34.3	34	6	AR100716	AR100716 Sequence
807	12.2	34.9	91	6	A69904	A69904 Sequence 33	880	12	34.3	36	6	A49575	A49575 Sequence 16
808	12.2	34.9	91	6	AR177635	AR177635 Sequence	881	12	34.3	36	6	AR075064	AR075064 Sequence
C 809	12.2	34.9	91	6	AR177636	AR177636 Sequence	882	12	34.3	36	6	AR141882	AR141882 Sequence
C 810	12.2	34.9	92	11	G68120	G68120 D7S3168 (CR	C 883	12	34.3	36	6	AX008920	AX008920 Sequence
811	12.2	34.9	93	6	A74464	A74464 Sequence 15	C 884	12	34.3	36	6	E16937	E16937 Linker DNA.
812	12.2	34.9	93	6	A77443	A77443 Sequence 15	C 885	12	34.3	37	6	A77194	A77194 Sequence 22
C 813	12.2	34.9	93	6	HUM7A4	129146 Homo sapien	C 886	12	34.3	37	6	AR003401	AR003401 Sequence
C 814	12.2	34.9	93	10	MMALDRED09	U89149 Mus musculu	887	12	34.3	37	6	AR003404	AR003404 Sequence
C 815	12.2	34.9	94	6	HSPHG12	U90257 Human Liver	C 888	12	34.3	37	6	I20229	I20229 Sequence 22
C 816	12.2	34.9	95	6	AX020435	AX020435 Sequence	C 889	12	34.3	37	6	I21190	I21190 Sequence 36
C 817	12.2	34.9	95	6	HSY17177	Y17177 Homo sapien	890	12	34.3	37	6	I21193	I21193 Sequence 39
C 818	12.2	34.9	96	6	AR014193	AR014193 Sequence	891	12	34.3	37	6	I74457	I74457 Sequence 39
C 819	12.2	34.9	96	6	AR041086	AR041086 Sequence	892	12	34.3	37	6	I74460	I74460 Sequence 39
C 820	12.2	34.9	96	6	AR060694	AR060694 Sequence	C 893	12	34.3	37	10	MUSTGDCG	MUSTGDCG
C 821	12.2	34.9	96	6	AR065127	AR065127 Sequence	C 894	12	34.3	38	6	AA1273	AA1273 Sequence 2
C 822	12.2	34.9	96	6	AR117016	AR117016 Sequence	C 895	12	34.3	39	6	AR060741	AR060741 Sequence
C 823	12.2	34.9	96	6	I35637	I35637 Sequence 25	896	12	34.3	39	6	AX149412	AX149412 Sequence
C 824	12.2	34.9	96	6	I64778	I64778 Sequence 3	C 897	12	34.3	39	6	AX207566	AX207566 Sequence
C 825	12.2	34.9	96	8	S42192	S42192 tRNA(Ser)CA	C 898	12	34.3	39	6	I28701	I28701 Sequence 4
C 826	12.2	34.9	96	9	HSTBX1054	AR033577 Homo sapi	C 899	12	34.3	40	6	AR024266	AR024266 Sequence
827	12.2	34.9	97	6	AR104339	AR104339 Sequence	C 900	12	34.3	40	6	AR026934	AR026934 Sequence
828	12.2	34.9	97	6	E00757	E00757 DNA sequenc	C 901	12	34.3	40	6	AR045119	AR045119 Sequence
829	12.2	34.9	97	6	E21611	E21611 Gene recomb	C 902	12	34.3	40	6	AR091820	AR091820 Sequence
830	12.2	34.9	97	6	E21619	E21619 Gene recomb	C 903	12	34.3	40	6	AR127655	AR127655 Sequence
831	12.2	34.9	97	6	E39805	E39805 Method for	C 904	12	34.3	40	6	AR157728	AR157728 Sequence
832	12.2	34.9	97	6	E40303	E40303 Method for	C 905	12	34.3	40	6	BD011343	BD011343 Chimeric
833	12.2	34.9	97	6	E62936	E62936 Method for	C 906	12	34.3	40	6	BD011343	BD011343 Chimeric
834	12.2	34.9	97	6	E64349	E64349 Method for	C 907	12	34.3	40	6	E43813	E43813 Chimeric an
C 835	12.2	34.9	99	6	AR147687	AR147687 Sequence	C 908	12	34.3	40	6	I75324	I75324 Sequence 73
C 836	12.2	34.9	100	3	RHERRE03	M80931 Rheostatica	909	12	34.3	41	12	SYNHYGROBI	SYNHYGROBI
C 837	12.2	34.9	100	6	AR142895	AR142895 Sequence	C 910	12	34.3	42	6	AR104006	AR104006 Sequence
C 838	12.2	34.9	100	9	HSEKRG5	U85838 Homo sapien	C 911	12	34.3	42	6	AR104073	AR104073 Sequence
C 839	12.2	34.9	100	11	HSPES2601	AL033906 H. sapiens	C 912	12	34.3	42	6	AR104074	AR104074 Sequence
840	12.2	34.9	19	6	AR117819	AR117819 Sequence	C 913	12	34.3	42	6	AR104075	AR104075 Sequence
841	12.2	34.3	19	6	AR149489	AR149489 Sequence	C 914	12	34.3	42	6	AR112493	AR112493 Sequence
842	12.2	34.3	20	6	A48137	A48137 Sequence 20	C 915	12	34.3	42	6	AR112499	AR112499 Sequence
843	12.2	34.3	20	6	AR177182	AR177182 Sequence	C 916	12	34.3	42	6	E34438	E34438 Inductive p
844	12.2	34.3	20	6	AX191145	AX191145 Sequence	C 917	12	34.3	42	6	E34434	E34434 Inductive p
C 845	12.2	34.3	20	6	AX293791	AX293791 Sequence	C 918	12	34.3	42	6	E50930	E50930 DNA and utl
C 846	12.2	34.3	21	6	AX259182	AX259182 Sequence	C 919	12	34.3	42	9	HSZA224225	HSZA224225 Homo sapi
847	12.2	34.3	21	6	AX098731	AX098731 Sequence	C 920	12	34.3	43	6	AR050692	AR050692 Sequence
848	12.2	34.3	23	6	AX136957	AX136957 Sequence	C 921	12	34.3	43	6	AX162810	AX162810 Sequence
849	12.2	34.3	24	6	AR148844	AR148844 Sequence	922	12	34.3	45	6	A03939	A03939 Nucleotide
850	12.2	34.3	24	6	AX085592	AX085592 Sequence	923	12	34.3	45	6	BD004189	BD004189 RNP deriv
C 851	12.2	34.3	24	6	AX164508	AX164508 Sequence	C 924	12	34.3	45	6	BD004190	BD004190 RNP deriv
C 852	12.2	34.3	24	6	AX289158	AX289158 Sequence	C 925	12	34.3	46	6	I20791	I20791 Sequence 4
C 853	12.2	34.3	25	6	BD006691	BD006691 Transport	C 926	12	34.3	47	6	AX194751	AX194751 Sequence
C 854	12.2	34.3	25	6	AX118036	AX118036 Sequence	927	12	34.3	48	6	AI00070	AI00070 Epstein-Bar
855	12.2	34.3	25	6	AX354423	AX354423 Sequence	C 928	12	34.3	48	6	A59392	A59392 Sequence 42
856	12.2	34.3	25	6	E02987	E02987 DNA encodin	C 929	12	34.3	48	6	AX155972	AX155972 Sequence
857	12.2	34.3	27	6	AA1161	AA1161 Sequence 8	930	12	34.3	48	6	E01063	E01063 DNA sequenc
C 858	12.2	34.3	27	6	AX114561	AX114561 Sequence	931	12	34.3	48	14	EBVCL1	X07814 EBV (B95-8)
C 859	12.2	34.3	28	6	AR025379	AR025379 Sequence	932	12	34.3	49	6	AX214215	AX214215 Sequence
C 860	12.2	34.3	28	6	AR053872	AR053872 Sequence	C 933	12	34.3	50	6	AX061571	AX061571 Sequence
861	12.2	34.3	28	6	AR090822	AR090822 Sequence	C 934	12	34.3	51	6	AR120170	AR120170 Sequence
862	12.2	34.3	28	6	AR174270	AR174270 Sequence	935	12	34.3	51	6	AR120177	AR120177 Sequence
863	12.2	34.3	28	6	AX259783	AX259783 Sequence	936	12	34.3	51	6	AR126168	AR126168 Sequence
864	12.2	34.3	28	6	AX350178	AX350178 Sequence	937	12	34.3	51	6	AR126175	AR126175 Sequence
865	12.2	34.3	28	6	AX350179	AX350179 Sequence	938	12	34.3	51	6	AR177984	AR177984 Sequence
866	12.2	34.3	28	6	AX350181	AX350181 Sequence	939	12	34.3	51	6	AR177991	AR177991 Sequence
867	12.2	34.3	28	6	AX350182	AX350182 Sequence	C 940	12	34.3	51	6	AX118037	AX118037 Sequence
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C 956	12	34.3	52	6	AR013865	AR013865 Sequence
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C 963	12	34.3	53	6	A62082	A62082 Sequence
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C 975	12	34.3	60	6	124289	124289 Sequence
C 976	12	34.3	66	6	AX288039	AX288039 Sequence
C 977	12	34.3	69	9	HSTRD43A	X14702 Human KT43A
C 978	12	34.3	70	6	AR012471	AR012471 Sequence
C 979	12	34.3	70	6	AR020299	AR020299 Sequence
C 980	12	34.3	70	6	AR109320	AR109320 Sequence
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C 986	12	34.3	71	6	AR165746	AR165746 Sequence
C 987	12	34.3	72	5	MARNR28D	1818736 Melanogramm
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C 994	12	34.3	77	6	144838	144838 Sequence
C 995	12	34.3	77	6	159522	159522 Sequence
C 996	12	34.3	78	1	MTTRNG	X06787 Methanobact
C 997	12	34.3	78	6	AX260827	AX260827 Sequence
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ALIGNMENTS

RESULT	1
LOCUS	G33119
DEFINITION	77 bp DNA linear STS 28-SEP-1996
ACCESSION	E979786L Human chromosome 11q13 STS Homo sapiens STS genomic, sequence tagged site.
VERSION	G33119
KEYWORDS	G33119.1 GI:2222864
SOURCE	STS.
ORGANISM	human.
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REFERENCE AUTHORS	
1 (bases 1 to 77)	
Guru, S.C., Olufemi, S.-E., Manickam, P., Cummings, C., Gieser, L.M., Pike, B.L., Bittner, M.L., Jiang, Y., Chinault, A.C., Nowak, N.J., Bizozowska, A., Cradlee, J.S., Wang, Y.-P., Koe, B.A., Weissmann, J.M., Boguski, M.S., Agarwal, S.K., Burns, A.L., Spiegel, A.M., Mats, S.J.,	

TITLE	Fleijter, W.L., de Jong, P.J., Collins, F.S. and Chandrasekharappa, S.C.
JOURNAL	A 2.8-Mb clone contig of the multiple endocrine neoplasia type 1
MEDLINE	(MEN1) region at 11q13
PUBMED	Genomics 42 (3), 436-445 (1997)
COMMENT	97349111
	9205115

Contact: Sirdanahalli C. Guru
Laboratory of Gene Transfer
National Human Genome Research Institute
NIH, Bethesda, MD 20892, USA
Email: sguru@nhgri.nih.gov
Primer A: ATGACGCAATGCTAAAGGGCAC
Primer B: AGTAAAGCGTGTGCACCTCCC
STS size: 77
PCR profile:

Presoak:	94 deg C-5min
Denaturation:	94 deg C-30sec
Annealing:	60 deg C-30sec
Polymerization:	72 deg C-1min
PCR cycles:	35
Final extension:	72 deg C-10min.
Location/Qualifiers	

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44	CATGGCAAGATGGGGAGAGGCACACCCCTTAC	76		

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LOCUS	AX157589	51 bp	DNA	linear
DEFINITION	Sequence 917 from Patent WO0140521.			
ACCESSION	AX157589			
VERSION	AX157589.1	GI:14538920		
KEYWORDS				
SOURCE	human.			

REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (pases 1 to 51)
Shinketsu, R. A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0140521-A 917 07-JUN-2001;
Curagen Corporation (US)

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misc.feature 6 a 20 c 19 g 6 t
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Best Local Similarity	71.98;	Pred. No. 1.2e+04;		

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Db	12	ttccctatgctgctgggacggggccgcctcagcttc	43						
RESULT	3								
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LOCUS	AX157591		51 bp	DNA		linear	PAT 22-JUN-2001		
DEFINITION	Sequence 919 from Patent WO0140521.								
ACCESSION	AX157591								
VERSION	AX157591.1	GI:14538922							
KEYWORDS									
SOURCE	human.								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
REFERENCE	1 (bases 1 to 51)								
AUTHORS	Shinkets,R.A. and Leach,M.								
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof								
JOURNAL	Patent: WO 0140521-A 919 07-JUN-2001;								
FEATURES	Curagen Corporation (US)								
Source	Location/Qualifiers								
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Db	10	ttccctatgctgctgggacggggccgcctcagcttc	41						
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AR120506			38 bp	DNA		linear	PAT 16-MAY-2001		
LOCUS	AR120506/c								
DEFINITION	Sequence 382 from patent US 6159469.								
ACCESSION	AR120506								
VERSION	AR120506.1	GI:14104082							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 38)								
	Choi,I.G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B.,								
	Fannon,M.R. and Rosen,C.A.								
TITLE	Streptococcus pneumoniae antigens and vaccines								
JOURNAL	Patent: US 6159469-A 382 12-DEC-2000;								
FEATURES	Location/Qualifiers								
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Qy	6	ctagaatgggagtggtcactcttgacc	35						
Db	32	ctagaatgctgtaaggcttaacgtcagctt	3						

[illegible]

[illegible]

TITLE	Nucleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods				
JOURNAL	Patent: US 5871962-A 124 16-FEB-1999;				
FEATURES	Location/Qualifiers				
source	1..42				
BASE COUNT	/organism="unknown"				
ORIGIN	7	a	13	c	13 g 9 t
Query Match	48.0%; Score 16.8; DB 6; Length 42;				
Best Local Similarity	75.0%; Pred. No. 2.7e+04;				
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Oy	1	catgtctagaatggagatggagtcactc	28		
Db	30	CATGTCGAGAAAGGCTGTGGGACCCCTC	3		
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LOCUS	120167/c	42 bp	DNA	Linear	PAT 07-OCT-1996
DEFINITION	Sequence	124	from patent	US 5514539.	
ACCESSION	120167				
VERSION	120167.1	GI:1600522			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 42)				
TITLE	Bukh,J., Miller,R.H. and Purcell,R.H.				
JOURNAL	Nucleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods and vaccines				
FEATURES	Patent: US 5514539-A 124 07-MAY-1996;				
Location/Qualifiers	1..42				
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Db	30	CATGTCGAGAAAGGCTGTGGGACCCCTC	3		
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DEFINITION	Human agammaglobulinemia-associated dysfunctional Ig rearranged heavy chain D-region (D-Xp1-0-H5) gene, clone lambda-XpB3.3.				
ACCESSION	M20417				
VERSION	M20417.1	GI:185152			
KEYWORDS	C-region; D-region; J-region; Immunoglobulin heavy chain; processed gene.				
SOURCE	Human bone marrow Epstein-Barr virus transformed precursor B cell line DNA, clone lambda-XpB3.3, from a patient with X-linked agammaglobulinemia.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 88)				
TITLE	Ichihara,Y., Matsuko,H., Tsuge,I., Okada,J.-I., Torii,S., Yasui,H. and Kurowsawa,Y.				
JOURNAL	Abnormalities in DNA rearrangements of immunoglobulin gene loci in precursor B cells derived from X-linked agammaglobulinemia patient and a severe combined immunodeficiency patient				

JOURNAL	Immunogenetics 27, 330-337 (1988)
MEDLINE	88186098
FEATURES	
SOURCE	Location/Qualifiers 1..88
ORGANISM	/organism="Homo sapiens"
BASE COUNT	18 a 15 c 24 g 31 t
ORIGIN	Chromosome 14q32.3.
Query Match	48.0%; Score 16.8; DB 9; Length 88;
Best Local Similarity	75.0%; Pred. No. 2.4e+04;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
Oy	4 gcttagaatgggagtggtcactctg 31 Db 2 GTTTGAAATGAGGTCCTGTGTCACCTGTGG 29
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AX343247	
LOCUS	AX343247 38 bp DNA linear PAT 01-FEB-2002
DEFINITION	Sequence 3 from Patent EP1170379.
ACCESSION	AX343247
VERSION	AX343247.1 GI:18491602
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	
AUTHORS	Gut,I.G., Lechner,D. and Sauer,S.
TITLE	Sample generation for genotyping by mass spectrometry
JOURNAL	Patent: EP 1170379-A 3 09-JAN-2002;
FEATURES	Location/Qualifiers 1..38
SOURCE	/organism="Homo sapiens"
BASE COUNT	9 a 11 c 12 g 6 t
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LOCUS	AX351627 38 bp DNA linear PAT 06-FEB-2002
DEFINITION	Sequence 3 from Patent WO0200931.
ACCESSION	AX351627
VERSION	AX351627.1 GI:18616910
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	
AUTHORS	Gut,I.G., Lechner,D. and Sauer,S.
TITLE	Sample generation for genotyping by mass spectrometry
JOURNAL	Patent: WO 0200931-A 3 03-JAN-2002;
FEATURES	Location/Qualifiers 1..38
SOURCE	/organism="Homo sapiens"
BASE COUNT	9 a 11 c 12 g 6 t

[illegible]

Best Local Similarity 72.48; Pred. No. 4.9e+04;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 34 CATTCTTAATGTCATGGATCCCTCT 6

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LOCUS	AX078730	36 bp	DNA	linear	PAT 22-FEB-2001
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DEFINITION Sequence 26 from Patent WO0107573.
ACCESSION AY070730

ACCESSION	AX078730	CT.1215925A
VERSION	AX078730 1	

VERSION AXU/8/30.1 GL:13158354

KEYWORDS

KEYWORDS	SOURCE
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BOOKS	synthetic construct
ORGANISM	synthetic construct

artificial sequence.

REFERENCE 1 (bases 1 to 36)

AUTHORS
Hauer, B., Schmid, R. L.

TITLE	Electron donor systems for the conversion of substrates
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Patent: WO 0107573-A
JOURNAL

JOURNAL
Patent: WO 010/373-2
BASE AKTIENGESellschaft

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ORIGIN

Query Match	46.38
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Best Local Similarity 72.48;

Matches 21; Conservative

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1 catgtctagaatggggatggg

Db 34 CATTCTTAAATGTCATGGG

[illegible]

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 05:39:59 ; Search time 369.89 Seconds
(without alignments)
162.459 Million cell updates/sec

Title: US-09-927-267-13

Perfect score: 35

Sequence: 1 catgtctagaatgaggatggtgctactctgacct 35

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

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Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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21: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.2	52.0	46	7	AA60796
2	17.6	50.3	51	22	AA173976
3	17.6	50.3	51	22	AA173978
4	17.2	49.1	38	18	AAV39899
5	17	48.6	58	18	AAV79289
6	16.8	48.0	42	16	AA083917
7	16.8	48.0	42	17	AA176577
8	16.4	46.9	50	22	AA133984
9	16.2	46.3	36	22	AA626235

C 10	16.2	46.3	36	22	AA626258
C 11	16.2	46.3	36	22	AA626260
C 12	16.2	46.3	36	22	AA626262
C 13	16.2	46.3	36	22	AA633314
C 14	16	45.7	51	22	AA173977
C 15	16	45.7	51	22	AA173979
C 16	16	45.7	93	22	ABA75975
C 17	16	45.7	93	22	ABA40538
C 18	16	45.7	93	22	AAK24653
C 19	16	45.7	93	22	AAK50650
C 20	16	45.7	93	22	AA127663
C 21	16	45.7	93	22	AA15631
C 22	15.6	44.6	60	24	ABA02187
C 23	15.6	44.6	88	15	AA074766
C 24	15.6	44.6	88	15	AA074766
C 25	15.4	44.0	51	22	AA175673
C 26	15.4	44.0	80	22	AA175673
C 27	15.4	44.0	81	16	AA06266
C 28	15.4	44.0	82	21	AAAC28035
C 29	15.4	44.0	86	21	AAA49668
C 30	15.4	44.0	98	21	AAAC22730
C 31	15.2	43.4	100	20	AAK5517
C 32	15.2	43.4	47	12	AAQ10271
C 33	15.2	43.4	51	22	AA127223
C 34	15.2	43.4	86	22	AAK19305
C 35	15.2	43.4	86	22	AAK45280
C 36	15.2	43.4	86	22	AA151233
C 37	15	42.9	25	21	AA236054
C 38	15	42.9	32	16	AA087423
C 39	15	42.9	32	16	AAH38568
C 40	14.8	42.3	47	21	AA259466
C 41	14.8	42.3	51	22	AA177485
C 42	14.8	42.3	58	22	AAAD1245
C 43	14.8	42.3	87	22	ABA72641
C 44	14.8	42.3	87	22	AAK47224
C 45	14.8	42.3	87	22	AA153060
C 46	14.8	42.3	96	22	ABA50062
C 47	14.8	42.3	96	22	ABA67998
C 48	14.8	42.3	96	22	ABA53036
C 49	14.8	42.3	96	22	AAK16393
C 50	14.8	42.3	96	22	AAK42140
C 51	14.8	42.3	96	22	AA122907
C 52	14.8	42.3	96	22	AA182205
C 53	14.8	42.3	96	22	AA108571
C 54	14.6	41.7	21	13	AA028770
C 55	14.6	41.7	33	24	AA171483
C 56	14.6	41.7	46	21	AAZ65189
C 57	14.6	41.7	46	22	AAAS12246
C 58	14.6	41.7	46	22	AAAS12253
C 59	14.6	41.7	46	22	AAAS12259
C 60	14.6	41.7	46	22	AAAS12265
C 61	14.6	41.7	46	22	AAAF4346
C 62	14.6	41.7	47	22	AAAS12260
C 63	14.6	41.7	50	22	AAH44830
C 64	14.6	41.7	50	23	ABLO1063
C 65	14.6	41.7	51	22	AA178456
C 66	14.6	41.7	55	21	AAAC29410
C 67	14.6	41.7	91	22	AAAF93138
C 68	14.6	41.7	91	22	AAAF93139
C 69	14.6	41.7	91	22	AAAF94555
C 70	14.6	41.7	95	22	AAAD02032
C 71	14.6	41.7	95	22	AAAD02033
C 72	14.4	41.1	20	21	AAZ77266
C 73	14.4	41.1	24	19	AAV02967
C 74	14.4	41.1	24	22	AA165074
C 75	14.4	41.1	28	18	AAV73525
C 76	14.4	41.1	28	18	AAV73544
C 77	14.4	41.1	30	20	AAV28029
C 78	14.4	41.1	39	11	AAO04933
C 79	14.4	41.1	47	23	AAH88357
C 80	14.4	41.1	48	20	AAK37602
C 81	14.4	41.1	48	20	AAK81786
C 82	14.4	41.1	48	20	AAK52313

B. megaterium BM-3
B. megaterium BM-3
Human neutropilin-1
Human silent SNP c
Human silent SNP c
Human foetal liver
Probe #19004 for g
Human brain expres
Human bone marrow
Probe #17596 for g
Arabidopsis ubiquitin
Human prepro-eryth
Human silent SNP c
PCR primer 2 used
HIV-1 reverse tran
Human secreted pro
HALO1, fragment of
Human secreted pro
Probe A(11) for bo
Human SNP oligonuc
Human brain expres
Human bone marrow
Probe #19919 used
Probe for mouse ML
Human GRK antisens
Human SNP flanking
Ig gamma 5' PCR pr
Human mmp-related
Human silent SNP c
E3-b1 primer used
Human foetal liver
Human bone marrow
Probe #21746 used
AA153060
Human breast cell
Human foetal liver
Probe #13502 for g
Human brain expres
Human bone marrow
Probe #12840 for g
Probe #16891 used
Probe #8562 used t
HIA class II gene
Human pax protein
Probe specific for
DNA encoding class
DNA encoding class
DNA encoding class
DNA encoding class
Human PRO109 hybr
DNA encoding class
Probe used to delete
Human SNP involvin
Human silent SNP c
Human secreted pro
Human HIV/tumorige
Human HIV/tumorige
Genetic suppressor
Synthetic oligo CM
Synthetic oligo CM
Human biallelic ma
Hepatitis GB virus
Androgen receptor
Primer RH107 for m
Primer RH107 for m
PCR primer for mam
Oligonucleotide ca
CMS disorder-relat
Human PRO245 hybr
Probe used to isol
Probe used to isol

83	14.4	41.1	48	21	AA058419	Human PRO245 (UNC2	156	13.8	39.4	59	21	AA296838	S. cerevisiae gene
84	14.4	41.1	48	21	AA077565	Human PRO245 hydri	157	13.8	39.4	60	18	AA062581	PCR primer for cys
85	14.4	41.1	48	21	AA252211	Hybridisation prob	158	13.8	39.4	60	21	AA053682	Oligonucleotide us
86	14.4	41.1	48	22	AA000166	Hybridisation prob	159	13.8	39.4	72	21	AA011529	Human secreted pro
87	14.4	41.1	48	22	AA072471	Human PRO polypept	160	13.8	39.4	80	22	ABA46642	Human breast cell
88	14.4	41.1	48	22	AA039149	Human PRO cDNA PCR	161	13.8	39.4	80	22	ABA64509	Human breast cell
89	14.4	41.1	48	22	AA097440	Human PRO245 hydri	162	13.8	39.4	80	22	ABA31647	Human foetal liver
90	14.4	41.1	50	22	AA033823	Human SNP oligonuc	163	13.8	39.4	80	22	AA012964	Probe #10113 for g
91	14.4	41.1	51	22	AA073275	Human silent SNP c	164	13.8	39.4	80	22	AA038692	Human brain expres
92	14.4	41.1	51	22	AA000814	Human amino acid c	165	13.8	39.4	80	22	AA019491	Human bone marrow
93	14.4	41.1	60	19	AA066662	Anti-human pas hum	166	13.8	39.4	80	22	AA044686	Probe #9424 for ge
94	14.4	41.1	60	21	AA078353	Humanised anti-Fas	167	13.8	39.4	80	22	AA010521	Probe #5210 used t
95	14.4	41.1	66	21	AA036385	PCR primer Jassm u	168	13.8	39.4	81	16	AA006278	HIV-1 reverse tran
96	14.4	41.1	66	22	AA016120	Human scfv gene VH	169	13.8	39.4	100	20	AA025515	Human interferon-a
97	14.4	41.1	99	7	AA061374	Synthetic regulati	170	13.6	38.9	20	20	AA097421	Primer used to amp
98	14.4	41.1	100	7	AA061373	Synthetic regulati	171	13.6	38.9	22	13	AA023615	Fig-PE-111non - a
99	14.2	40.6	20	20	AA023258	PCR primer used to	172	13.6	38.9	28	21	AA0296713	T cell antigen rec
100	14.2	40.6	26	20	AA088015	Calcium channel al	173	13.6	38.9	30	22	AA067240	Fibrosis modulator
101	14.2	40.6	30	20	AA078116	HLA-G/HLA-B*5801 c	174	13.6	38.9	31	20	AA024576	Human SR-BI gene e
102	14.2	40.6	33	12	AA011003	HIV-1 gag region s	175	13.6	38.9	31	20	AA024578	Human SR-BI gene e
103	14.2	40.6	34	18	AA061113	Chimeric chemokine	176	13.6	38.9	31	20	AA024668	Human SR-BI gene e
104	14.2	40.6	39	22	AA084965	Nucleotide sequenc	177	13.6	38.9	31	20	AA024670	Human SR-BI gene e
105	14.2	40.6	51	22	AA090467	Human clone c94396	178	13.6	38.9	32	17	AA046094	5' primer for CD34
106	14.2	40.6	62	14	AA040739	Delta TCR V-J Junc	179	13.6	38.9	34	22	AA045159	Human proliprote
107	14.2	40.6	80	22	ABA48874	Human breast cell	180	13.6	38.9	36	11	AA006488	Human intestinal m
108	14.2	40.6	80	22	ABA65793	Human foetal liver	181	13.6	38.9	36	21	AA035698	Permutelin Linker e
109	14.2	40.6	80	22	ABA33853	Probe #12319 for g	182	13.6	38.9	40	20	AA026953	Human chromosome 1
110	14.2	40.6	80	22	AA015222	Human brain expres	183	13.6	38.9	40	22	AA017939	Caenor o11 plant p
111	14.2	40.6	80	22	AA040946	Human bone marrow	184	13.6	38.9	41	19	AA050960	Maize polymorphic
112	14.2	40.6	80	22	AA012173	Probe #11646 for g	185	13.6	38.9	41	19	AA050961	Maize polymorphic
113	14.2	40.6	80	22	AA017000	Probe #15686 used t	186	13.6	38.9	42	14	AA048151	Lambda gut-t6s ter
114	14.2	40.6	80	22	AA0107401	Probe #7392 used t	187	13.6	38.9	42	19	AA005413	Primer used in pro
115	14.2	40.6	84	11	AA005273	Sequence encoding	188	13.6	38.9	42	21	AA073395	Oligonucleotide UC
116	14.2	40.6	84	11	AA005482	Hepatitis GB virus	189	13.6	38.9	42	21	AA055883	Yeast URA3 gene PC
117	14	40.0	29	16	AA097822	Primer 1502 to det	190	13.6	38.9	48	16	AA085485	OMTKY3(6-56) analo
118	14	40.0	29	16	AA003448	PrP-APP fusion DNA	191	13.6	38.9	50	22	AA030297	Human SNP oligonuc
119	14	40.0	31	21	AA078817	Human genomic DNA	192	13.6	38.9	50	22	AA013491	Human SNP oligonuc
120	14	40.0	33	20	AA091526	Bovine Interferon-	193	13.6	38.9	51	21	AA064786	C. trachomatis pmp
121	14	40.0	72	24	AA098490	Human protective D	194	13.6	38.9	51	22	AA017879	Human silent SNP c
122	14	40.0	73	24	AA098927	Human prostate can	195	13.6	38.9	51	22	AA056289	C. Chlamydia trachoma
123	14	40.0	79	16	AA000267	Full length bFGF f	196	13.6	38.9	61	18	AA057875	L-scleritin orphan
124	14	40.0	79	16	AA070842	bFGF family 1 ligat	197	13.6	38.9	69	11	AA006489	Human intestinal m
125	14	40.0	86	17	AA088612	VBSF nucleic acid	198	13.6	38.9	75	22	ABA75877	Human foetal liver
126	14	40.0	96	14	AA038887	gH1 variable domai	199	13.6	38.9	75	22	ABA40442	Probe #18908 for g
127	14	40.0	96	18	AA085863	CDR-grafted heavy	200	13.6	38.9	75	22	AA024558	Human brain expres
128	14	40.0	96	21	AA046922	gH1 variable domai	201	13.6	38.9	75	22	AA050551	Human bone marrow
129	14	40.0	96	24	AA098489	Human protective D	202	13.6	38.9	75	22	AA0127562	Probe #17495 for g
130	13.8	39.4	20	16	AA081357	Human gene signatu	203	13.6	38.9	75	22	AA0156534	Probe #25220 used
131	13.8	39.4	30	17	AA070247	Yeast alpha-mating	204	13.6	38.9	83	22	ABA47673	Human breast cell
132	13.8	39.4	30	21	AA057463	Kunitz protease in	205	13.6	38.9	83	22	ABA65568	Human foetal liver
133	13.8	39.4	30	22	AA014245	Oligonucleotide 62	206	13.6	38.9	83	22	ABA32657	Probe #11123 for g
134	13.8	39.4	31	20	AA020235	Brassica raifinose	207	13.6	38.9	83	22	AA013972	Human brain expres
135	13.8	39.4	31	22	AA090290	Primer Ad5RI used	208	13.6	38.9	83	22	AA039718	Human bone marrow
136	13.8	39.4	38	21	AA029436	PCR primer J0140 f	209	13.6	38.9	83	22	AA0120525	Probe #10458 for g
137	13.8	39.4	39	21	AA053708	Oligonucleotide us	210	13.6	38.9	83	22	AA0145734	Probe #14420 used t
138	13.8	39.4	41	19	AA050753	Brassica sp. polym	211	13.6	38.9	83	22	AA0106223	Probe #6214 used t
139	13.8	39.4	43	13	AA033896	Brassica sp. polym	212	13.6	38.9	87	21	AA010414	Human secreted pro
140	13.8	39.4	43	19	AA033896	Sequence upstream	213	13.6	38.9	88	22	AA072826	Human foetal liver
141	13.8	39.4	47	21	AA069926	Human map-related	214	13.6	38.9	88	22	ABA38442	Probe #16908 for g
142	13.8	39.4	50	15	AA069782	Hepes simplex vir	215	13.6	38.9	88	22	AA021257	Human brain expres
143	13.8	39.4	50	18	AA064244	HSV-2 g'g/c (start	216	13.6	38.9	88	22	AA023783	Human brain expres
144	13.8	39.4	50	20	AA017532	Test sequence from	217	13.6	38.9	88	22	AA047414	Human bone marrow
145	13.8	39.4	50	22	AA017532	Human SNP oligonuc	218	13.6	38.9	88	22	AA012933	Probe #15866 for g
146	13.8	39.4	51	22	AA0330024	Human SNP oligonuc	219	13.6	38.9	88	22	AA0126981	Probe #16914 for g
147	13.8	39.4	51	22	AA033009	Human SNP oligonuc	220	13.6	38.9	88	22	AA0153251	Probe #21937 used
148	13.8	39.4	51	22	AA0174208	Human silent SNP c	221	13.6	38.9	89	20	AA082653	Oligonucleotide us
149	13.8	39.4	51	22	AA0175672	Human silent SNP c	222	13.6	38.9	100	22	AA071772	Human immune/haema
150	13.8	39.4	51	22	AA0179476	Human DNA containi	223	13.4	38.3	18	22	AA095046	Human Otoferrlin ex
151	13.8	39.4	53	21	AA071022	Molecular interact	224	13.4	38.3	19	21	AA066236	Dog genomic marker
152	13.8	39.4	53	21	AA071023	Molecular interact	225	13.4	38.3	23	21	AA007740	Human lysoenzyme L
153	13.8	39.4	53	21	AA071035	Molecular interact	226	13.4	38.3	24	21	AA051487	Primer DcATxbat fo
154	13.8	39.4	53	21	AA071036	Molecular interact	227	13.4	38.3	25	21	AA004833	Chicken leptin rec
155	13.8	39.4	59	12	AA013344	MuHIV DNA insert	228	13.4	38.3	26	19	AA029144	Homio sapiens DNase

229	13.4	38.3	28	20	AA06922	Canine factor VIII	c 302	13.2	37.7	50	22	AA133751	Human SNP oligonuc
230	13.4	38.3	28	21	AA256616	Canine Factor VIII	c 303	13.2	37.7	51	16	AA05645	Human factor VIII
231	13.4	38.3	30	20	AA081616	HTPr sequence-spec	c 304	13.2	37.7	51	22	AA128693	Human SNP oligonuc
c 232	13.4	38.3	32	22	AAH22591	Mutant Bcl-Gs cons	c 305	13.2	37.7	51	22	AA129077	Human SNP oligonuc
233	13.4	38.3	33	22	AA082360	Human G protein co	c 306	13.2	37.7	51	22	AA133022	Human SNP oligonuc
234	13.4	38.3	33	22	AA086986	Human novel G-prot	c 307	13.2	37.7	51	22	AA176256	Human silent SNP c
c 235	13.4	38.3	39	19	AAV36562	Self-cleaving clas	c 308	13.2	37.7	51	22	AA177482	Human silent SNP c
c 236	13.4	38.3	40	21	AAA10269	PSMA monoclonal an	c 309	13.2	37.7	51	22	AA177484	Human silent SNP c
c 237	13.4	38.3	40	21	AA295969	POLYnucleotide seq	c 310	13.2	37.7	51	22	AA070006	Human type I colla
238	13.4	38.3	40	21	AA166610	Human leukotriene	c 311	13.2	37.7	51	22	AA084757	PCR primer used to
239	13.4	38.3	41	14	AA057536	PCR primer CLC 27	c 312	13.2	37.7	51	23	ABL00763	Human amino acid c
240	13.4	38.3	46	15	AA062708	Primer for amplifi	c 313	13.2	37.7	52	20	AA077575	Adenovirus major I
241	13.4	38.3	50	22	AA131317	Human SNP oligonuc	c 314	13.2	37.7	52	20	AA077586	Adenovirus wild ty
242	13.4	38.3	50	22	AA089629	Human isomerase co	c 315	13.2	37.7	52	20	AA077588	Adenovirus MLP mut
243	13.4	38.3	50	22	AA089631	Human isomerase co	c 316	13.2	37.7	52	21	AAA54335	Primer for amplify
c 244	13.4	38.3	50	22	AA089633	Human isomerase co	c 317	13.2	37.7	53	21	AA092866	PCR primer E for a
c 245	13.4	38.3	50	24	AA017560	MOMIV envelope gly	c 318	13.2	37.7	60	22	AA026974	Human oestrogen re
c 246	13.4	38.3	51	22	AA127758	Human SNP oligonuc	c 319	13.2	37.7	62	15	AA070954	CYP 1A1 gene speci
c 247	13.4	38.3	51	22	AA175439	Human silent SNP c	c 320	13.2	37.7	63	21	AAA92491	Adenovirus major 1
c 248	13.4	38.3	51	22	AA175796	Human silent SNP c	c 321	13.2	37.7	64	18	AA076875	Staphylococcus aur
249	13.4	38.3	51	22	AA089334	Human DNA/RNA bind	c 322	13.2	37.7	64	21	AAA92492	Adenovirus major 1
250	13.4	38.3	55	14	AA076715	Primer for constru	c 323	13.2	37.7	77	22	AA073974	Human foetal liver
251	13.4	38.3	56	22	AA090939	Human inflammatory	c 324	13.2	37.7	77	22	AA072427	Human brain expres
252	13.4	38.3	59	21	AA048288	Oligonucleotide Sig	c 325	13.2	37.7	77	22	AA048594	Human bone marrow
c 253	13.4	38.3	60	21	AA071969	Rat hepatocyte car	c 326	13.2	37.7	77	22	AA154423	Full length bFGF f
c 254	13.4	38.3	79	21	AA087271	Human secreted pro	c 327	13.2	37.7	79	16	AA070073	bFGF family 1 lig
255	13.4	38.3	81	22	AA032282	Human foetal liver	c 328	13.2	37.7	84	17	AA073988	Islet regenerating
256	13.4	38.3	81	22	ABA075640	Probe #18715 for g	c 329	13.2	37.7	84	20	AA033765	Mouse islet regene
257	13.4	38.3	81	22	ABA040249	Human brain expres	c 330	13.2	37.7	84	20	AA033765	Mouse islet regene
258	13.4	38.3	81	22	AA042424	Human bone marrow	c 331	13.2	37.7	84	20	AA033765	P13 consensus nucl
259	13.4	38.3	81	22	AA050277	Probe #17285 for g	c 332	13.2	37.7	84	21	AAA99689	SEQ ID NO: 9 for 1
260	13.4	38.3	81	22	AA127352	Probe #24925 used	c 333	13.2	37.7	84	21	AAA99718	Mouse body weight
261	13.4	38.3	81	22	AA156239	gGMP-specific apta	c 334	13.2	37.7	85	13	AAA52256	Mouse islet regen
262	13.4	38.3	90	22	AA016702	Human secreted pro	c 335	13.2	37.7	85	21	AA034112	Sequence upstream
c 263	13.4	38.3	93	21	AA016714	Human foetal liver	c 336	13.2	37.7	85	21	AA060461	Murine factor V 5'
c 264	13.4	38.3	94	22	ABA071979	Human MN promoter	c 337	13.2	37.7	86	18	AA030120	Sequence of the tr
c 265	13.2	37.7	20	21	AA052541	Human ribosomal p	c 338	13.2	37.7	87	14	AA079022	Rous sarcoma virus
c 266	13.2	37.7	21	22	AA033916	Antisense PCR prim	c 339	13.2	37.7	90	21	AA066495	Chimeric receptor
c 267	13.2	37.7	21	22	AA0500287	PCR primer #2, use	c 340	13.2	37.7	90	21	AA068023	Oligonucleotide A9
c 268	13.2	37.7	21	22	AA089036	Protein disulfide	c 341	13.2	37.7	90	22	AA044869	Oligonucleotide fo
c 269	13.2	37.7	23	18	AA060088	SMCX primer PRH2	c 342	13.2	37.7	90	22	AA044869	Human primary sign
270	13.2	37.7	27	19	AA099659	Human Factor-VIII	c 343	13.2	37.7	90	22	AA044869	Human primary sign
c 271	13.2	37.7	27	20	AA083524	Primer Up FR Apai	c 344	13.2	37.7	90	22	AA044869	Human primary sign
c 272	13.2	37.7	27	20	AA089018	Alzheimer's diseas	c 345	13.2	37.7	90	22	AA044869	Human primary sign
273	13.2	37.7	28	14	AA053422	SIVmac/HIV-1 junct	c 346	13.2	37.7	90	22	AA044869	Human primary sign
274	13.2	37.7	28	14	AA053426	SIVmac/HIV-1 junct	c 347	13.2	37.7	90	22	AA044869	Human primary sign
c 275	13.2	37.7	31	21	AA046627	Primer 2087-37 for	c 348	13.2	37.7	90	22	AA044869	Human primary sign
276	13.2	37.7	31	16	AA087997	Bombesin-related p	c 349	13.2	37.7	90	22	AA044869	Human primary sign
277	13.2	37.7	33	22	AA016598	Human ribosomal p	c 350	13.2	37.7	90	22	AA044869	Human primary sign
278	13.2	37.7	33	22	AA048156	Human aminoacyl-tr	c 351	13.2	37.7	90	22	AA044869	Human primary sign
279	13.2	37.7	34	22	AA046478	Ribosome S7 prot	c 352	13.2	37.7	90	22	AA044869	Human primary sign
280	13.2	37.7	40	16	AA084799	Sphocerebellar at	c 353	13.2	37.7	90	22	AA044869	Human primary sign
281	13.2	37.7	40	21	AA056818	Reverse PCR primer	c 354	13.2	37.7	90	22	AA044869	Human primary sign
282	13.2	37.7	40	21	AA036110	POLYnucleotide seq	c 355	13.2	37.7	90	22	AA044869	Human primary sign
c 283	13.2	37.7	41	19	AA047777	Maize polymorphic	c 356	13.2	37.7	90	22	AA044869	Human primary sign
c 284	13.2	37.7	41	19	AA047778	Maize polymorphic	c 357	13.2	37.7	90	22	AA044869	Human primary sign
c 285	13.2	37.7	41	24	AA021313	Lactococcus lactis	c 358	13.2	37.7	90	22	AA044869	Human primary sign
286	13.2	37.7	41	24	AA021313	Lactococcus lactis	c 359	13.2	37.7	90	22	AA044869	Human primary sign
287	13.2	37.7	41	24	AA021313	Lactococcus lactis	c 360	13.2	37.7	90	22	AA044869	Human primary sign
288	13.2	37.7	42	19	AA016870	Human pax protein	c 361	13.2	37.7	90	22	AA044869	Human primary sign
289	13.2	37.7	42	19	AA016870	Human pax protein	c 362	13.2	37.7	90	22	AA044869	Human primary sign
c 290	13.2	37.7	43	20	AA021333	HLA-DR2 beta chain	c 363	13.2	37.7	90	22	AA044869	Human primary sign
c 291	13.2	37.7	43	20	AA021333	Lactococcus lactis	c 364	13.2	37.7	90	22	AA044869	Human primary sign
c 292	13.2	37.7	43	20	AA021333	Lactococcus lactis	c 365	13.2	37.7	90	22	AA044869	Human primary sign
c 293	13.2	37.7	43	16	AA087996	Bombesin-related p	c 366	13.2	37.7	90	22	AA044869	Human primary sign
294	13.2	37.7	45	21	AA051468	Maize ZmKCS1 part1	c 367	13.2	37.7	90	22	AA044869	Human primary sign
295	13.2	37.7	50	15	AA069829	Adenovirus type-2	c 368	13.2	37.7	90	22	AA044869	Human primary sign
296	13.2	37.7	50	15	AA069830	Adenovirus type-5	c 369	13.2	37.7	90	22	AA044869	Human primary sign
297	13.2	37.7	50	18	AA064291	Adenovirus type 2	c 370	13.2	37.7	90	22	AA044869	Human primary sign
298	13.2	37.7	50	18	AA064292	Adenovirus type 5	c 371	13.2	37.7	90	22	AA044869	Human primary sign
299	13.2	37.7	50	20	AA017580	Test sequence from	c 372	13.2	37.7	90	22	AA044869	Human primary sign
300	13.2	37.7	50	20	AA017580	Test sequence from	c 373	13.2	37.7	90	22	AA044869	Human primary sign
c 301	13.2	37.7	50	21	AA099385	PCR primer A for a	c 374	13.2	37.7	90	22	AA044869	Human primary sign

C 375	13	37.1	50	22	AA133698	Human SNP oligonuc	C 448	12.8	36.6	24	16	AA105652	Primer 336-2, sens
C 376	13	37.1	51	22	AAH90602	Human clone c94392	449	12.8	36.6	24	24	AB188060	Capture oligonucle
C 377	13	37.1	51	22	AA130393	Human SNP oligonuc	C 450	12.8	36.6	24	24	AB188061	Capture oligonucle
C 378	13	37.1	51	22	AA130432	Human SNP oligonuc	C 451	12.8	36.6	25	16	AA105651	Primer 336-1, sens
C 379	13	37.1	51	22	AA173602	Human silent SNP c	C 452	12.8	36.6	25	19	AAV37049	PCR primer for ant
C 380	13	37.1	51	22	AA175256	Human silent SNP c	C 453	12.8	36.6	25	19	AAV37049	PCR primer for ant
C 381	13	37.1	51	22	AA175258	Human silent SNP c	C 454	12.8	36.6	26	21	AAAC61933	PCR primer for DNA
C 382	13	37.1	51	22	AA175260	Human silent SNP c	C 455	12.8	36.6	26	21	AAAC61933	Synechocystis pote
C 383	13	37.1	51	22	AA175261	Human silent SNP c	C 456	12.8	36.6	27	21	AAZ60364	RACE primer used t
C 384	13	37.1	51	22	AA178457	Human silent SNP c	C 457	12.8	36.6	27	21	AAZ60365	RACE primer used t
C 385	13	37.1	54	15	AA068303	Primer 6 NO11 VL-1	C 458	12.8	36.6	27	21	AAZ54649	Neisseria species
C 386	13	37.1	56	17	AA133474	Self-sterilizing P	C 459	12.8	36.6	30	20	AAV02614	Human BI PCR prime
C 387	13	37.1	56	20	AAV83933	Oligonucleotide HR	C 460	12.8	36.6	31	19	AAV67597	Nucleotide fragmen
C 388	13	37.1	59	19	AAV54296	Primer JMTCR204 us	C 461	12.8	36.6	31	20	AAV06291	Human bi-allelic po
C 389	13	37.1	59	20	AAV55378	Soluble sc-TCR fus	C 462	12.8	36.6	31	22	AA130614	Human single nucle
C 390	13	37.1	60	24	AAV17435	Human p62 reverse	C 463	12.8	36.6	32	19	AAV15468	PR-1 promoter prim
C 391	13	37.1	62	17	AA114647	7AR-3 3' DNA prime	C 464	12.8	36.6	32	21	AAV61196	PCR primer #1 used
C 392	13	37.1	66	20	AAV36825	PCR primer for con	C 465	12.8	36.6	32	22	AAV10693	Sense PCR primer u
C 393	13	37.1	70	20	AAV76996	Chimeric oligonuc	C 466	12.8	36.6	33	33	AAV04910	Amplification cont
C 394	13	37.1	71	17	AA133475	Self-sterilizing P	C 467	12.8	36.6	33	24	ABA92622	Human class II ant
C 395	13	37.1	71	20	AAV83934	Oligonucleotide HR	C 468	12.8	36.6	37	21	AAV62415	Agrobacterium Ti-p
C 396	13	37.1	72	18	AAV65210	Transforming growt	C 469	12.8	36.6	38	21	AAV54382	Primer for signal
C 397	13	37.1	72	22	AAV61882	Maize invertase DN	C 470	12.8	36.6	39	15	AAQ70170	Reverse PCR primer
C 398	13	37.1	73	18	AAV57920	L-selectin family	C 471	12.8	36.6	40	15	AAQ62533	Oligonucleotide pr
C 399	13	37.1	73	20	AAV32746	Human DCR3 EST seq	C 472	12.8	36.6	41	20	AAZ21292	Lactococcus lactis
C 400	13	37.1	80	14	AAQ46871	Ovine GHG primer O	C 473	12.8	36.6	41	20	AAZ21294	Lactococcus lactis
C 401	13	37.1	81	19	AAV01623	Insecticidal gene	C 474	12.8	36.6	41	20	AAZ21300	Lactococcus lactis
C 402	13	37.1	81	22	AAV73319	Oligonucleotide #1	C 475	12.8	36.6	41	20	AAZ21303	Lactococcus lactis
C 403	13	37.1	83	22	AAV76105	Human foetal liver	C 476	12.8	36.6	42	19	AAV19920	PCR primer for Con
C 404	13	37.1	83	22	ABA40660	Probe #19126 for g	C 477	12.8	36.6	45	22	AAAD19773	Human hG-CSF DNA 5
C 405	13	37.1	83	22	AAK22973	Human brain expres	C 478	12.8	36.6	45	22	AAH26512	Low density Lipopr
C 406	13	37.1	83	22	AAK24781	Human brain expres	C 479	12.8	36.6	47	21	AAZ66341	Human map-related
C 407	13	37.1	83	22	AAK49147	Human bone marrow	C 480	12.8	36.6	47	21	AAZ69023	Human cystatin C p
C 408	13	37.1	83	22	AAK50776	Human bone marrow	C 481	12.8	36.6	48	24	AA168747	Staphylococcus aur
C 409	13	37.1	83	22	AAI27793	Probe #17726 for g	C 482	12.8	36.6	50	18	AAV76334	Human clone c94253
C 410	13	37.1	83	22	AAI54978	Probe #23664 used	C 483	12.8	36.6	50	21	AAV76950	Human clone c94401
C 411	13	37.1	83	22	AAI56765	Probe #25451 used	C 484	12.8	36.6	50	21	AAV77327	Human clone c94401
C 412	13	37.1	86	22	ABA71873	Human foetal liver	C 485	12.8	36.6	50	22	AA133576	Human SNP oligonuc
C 413	13	37.1	86	22	ABA71915	Probe #16381 for g	C 486	12.8	36.6	50	22	AA133576	Human SNP oligonuc
C 414	13	37.1	86	22	AAK20250	Human brain expres	C 487	12.8	36.6	51	18	AAV59918	Oligonucleotide pr
C 415	13	37.1	86	22	AAK46320	Human bone marrow	C 488	12.8	36.6	51	21	AAV76881	Human clone c93951
C 416	13	37.1	86	22	AAI25613	Probe #15546 for g	C 489	12.8	36.6	51	21	AAV76948	Human clone c94253
C 417	13	37.1	86	22	AAI52219	Probe #20905 used	C 490	12.8	36.6	51	21	AAV77364	Human clone c94491
C 418	13	37.1	87	7	AAH60663	HIV virus gag regi	C 491	12.8	36.6	51	22	AA126832	Human SNP oligonuc
C 419	13	37.1	87	20	AAH85383	WHL rabbit athero	C 492	12.8	36.6	51	22	AA127065	Human SNP oligonuc
C 420	13	37.1	87	22	ABA47213	Human breast cell	C 493	12.8	36.6	51	22	AA127438	Human SNP oligonuc
C 421	13	37.1	87	22	ABA65097	Human foetal liver	C 494	12.8	36.6	51	22	AA130552	Human SNP oligonuc
C 422	13	37.1	87	22	ABA32202	Probe #10668 for g	C 495	12.8	36.6	51	22	AA133121	Human SNP oligonuc
C 423	13	37.1	87	22	AAK13519	Human brain expres	C 496	12.8	36.6	51	22	AA173274	Human silent SNP c
C 424	13	37.1	87	22	AAK39258	Human bone marrow	C 497	12.8	36.6	51	22	AA173956	Human silent SNP c
C 425	13	37.1	87	22	AAI20069	Probe #10002 for g	C 498	12.8	36.6	51	22	AA174605	Human silent SNP c
C 426	13	37.1	87	22	AAI45267	Probe #13953 used	C 499	12.8	36.6	51	22	AA177348	Human silent SNP c
C 427	13	37.1	87	22	AAI05776	Probe #5767 used t	C 500	12.8	36.6	51	22	AA177480	Human silent SNP c
C 428	13	37.1	91	22	AAI47042	Probe #15728 used	C 501	12.8	36.6	51	22	AA177481	Human silent SNP c
C 429	13	37.1	94	18	AAI58019	P-selectin SELX 2	C 502	12.8	36.6	51	22	AA177657	Human silent SNP c
C 430	13	37.1	96	15	AAQ78190	Recombinant PDGF B	C 503	12.8	36.6	51	22	AA178245	Human silent SNP c
C 431	13	37.1	97	22	ABA74548	Human foetal liver	C 504	12.8	36.6	51	22	AA179039	Human silent SNP c
C 432	13	37.1	97	22	ABA39363	Probe #17829 for g	C 505	12.8	36.6	51	22	AAH89319	Human angiotensin
C 433	13	37.1	97	22	AAK23015	Human brain expres	C 506	12.8	36.6	51	22	AAH90601	Human clone c94392
C 434	13	37.1	97	22	AAK49192	Human bone marrow	C 507	12.8	36.6	51	22	AAH96626	Human DNA contain
C 435	13	37.1	97	22	AAI55027	Probe #23713 used	C 508	12.8	36.6	51	23	AB100531	Human silent nonco
C 436	13	37.1	98	9	AAH81203	Recombinant platelet	C 509	12.8	36.6	54	22	AAAD07008	Human type I colla
C 437	13	37.1	98	14	AAQ48657	PDGF Bc-sis precur	C 510	12.8	36.6	54	22	AAH84759	PCR primer used to
C 438	13	37.1	100	22	AAV29969	Human lung antigen	C 511	12.8	36.6	59	20	AAH8041	Primer for rat GAB
C 439	12.8	36.6	20	20	AAV30825	Human Smad6 antisense	C 512	12.8	36.6	59	21	AAZ51427	PCR primer for M-23 t
C 440	12.8	36.6	20	20	AAV30826	Human Smad6 sense	C 513	12.8	36.6	60	18	AAV96763	Human F-Cadherin v
C 441	12.8	36.6	20	21	AAZ93632	Antisense oligonuc	C 514	12.8	36.6	60	19	AAV45268	Heregulin-beta3 EG
C 442	12.8	36.6	20	22	AAH27677	Human bel-x antisense	C 515	12.8	36.6	60	19	AAV66660	Anti-human Fas hum
C 443	12.8	36.6	21	21	AAV75650	Human bi-allelic ma	C 516	12.8	36.6	60	19	AAV60528	Cloned Factor X-bi
C 444	12.8	36.6	21	21	AAV50117	Human serine prote	C 517	12.8	36.6	60	19	AAV21324	Immunoglobulin I g
C 445	12.8	36.6	22	21	AAZ46336	Human zkuns Kunitz	C 518	12.8	36.6	60	19	AAV21325	Immunoglobulin I g
C 446	12.8	36.6	22	22	AAAD14335	Human zkuns DNA am	C 519	12.8	36.6	60	19	AAV21363	Immunoglobulin genom
C 447	12.8	36.6	23	18	AAV49421	Banana bunchy top	C 520	12.8	36.6	60	19	AAV21371	Immunoglobulin genom

C 521	12.8	36.6	60	19	AAV21318	Immunoglobulin I m	C 594	12.6	36.0	45	21	AAA07129	S. pyogenes cystei
C 522	12.8	36.6	60	21	AAA78351	Humanised anti-Fas	C 595	12.6	36.0	45	21	AAA07138	S. pyogenes cystei
C 523	12.8	36.6	60	21	AA51958	Camine von Willibr	C 596	12.6	36.0	45	21	AA07144	S. pyogenes cystei
C 524	12.8	36.6	60	21	AA237453	Coding sequence fo	C 597	12.6	36.0	47	16	AA093293	Family 3 DGE 2'-N
C 525	12.8	36.6	61	17	AA229759	D10 scfcr hexahist	C 598	12.6	36.0	47	21	AA268329	Human map-related
C 526	12.8	36.6	62	22	AAH45396	Synthetic DNA sequ	C 599	12.6	36.0	47	22	AAE70674	2'NH2 RNA ligand t
C 527	12.8	36.6	63	16	AAAT21813	Human gene signatu	C 600	12.6	36.0	47	23	AAH88414	CNS disorder-relat
C 528	12.8	36.6	64	18	AAAT6183	Staphylococcus aur	C 601	12.6	36.0	47	23	AAH88663	CNS disorder-relat
C 529	12.8	36.6	65	18	AAV76989	Staphylococcus aur	C 602	12.6	36.0	50	22	AAI28743	Human SNP oligonuc
C 530	12.8	36.6	70	19	AAV40088	Oligonucleotide R1	C 603	12.6	36.0	50	22	AAI30120	Human SNP oligonuc
C 531	12.8	36.6	70	19	AAV40089	Oligonucleotide F1	C 604	12.6	36.0	50	22	AAI30121	Human SNP oligonuc
C 532	12.8	36.6	71	18	AAAT78610	Class I SLELEX gene	C 605	12.6	36.0	51	22	AAI27252	Human SNP oligonuc
C 533	12.8	36.6	71	18	AAAT82655	Oligonucleotide us	C 606	12.6	36.0	51	22	AAI27387	Human SNP oligonuc
C 534	12.8	36.6	74	16	AAAT20769	Human gene signatu	C 607	12.6	36.0	51	22	AAI28188	Human SNP oligonuc
C 535	12.8	36.6	81	16	AAQ94942	Single chain Fv fr	C 608	12.6	36.0	51	22	AAI30482	Human SNP oligonuc
C 536	12.8	36.6	81	22	ABA71983	Human foetal liver	C 609	12.6	36.0	51	22	AAI33357	Human SNP oligonuc
C 537	12.8	36.6	81	22	ABA37925	Probe #16391 for g	C 610	12.6	36.0	51	22	AAI74635	Human silent SNP c
C 538	12.8	36.6	81	22	AAK20275	Human brain expres	C 611	12.6	36.0	51	22	AAI75017	Human silent SNP c
C 539	12.8	36.6	81	22	AAK46349	Human bone marrow	C 612	12.6	36.0	51	22	AAI77007	Human silent SNP c
C 540	12.8	36.6	81	22	AAI25623	Probe #15556 for g	C 613	12.6	36.0	51	22	AAI78163	Human silent SNP c
C 541	12.8	36.6	81	22	AAI52245	Probe #20931 used	C 614	12.6	36.0	51	22	AAI79066	Human silent SNP c
C 542	12.8	36.6	86	21	AA25234	Human secreted pro	C 615	12.6	36.0	51	22	AAH89232	Human elastase inh
C 543	12.8	36.6	90	21	AA29282	Human secreted pro	C 616	12.6	36.0	51	22	AAH89415	Human coding sequ
C 544	12.8	36.6	92	22	ABA75462	Human foetal liver	C 617	12.6	36.0	51	22	AAH90468	Human clone cg4396
C 545	12.8	36.6	92	22	ABA40087	Probe #18553 for g	C 618	12.6	36.0	51	22	AAH37984	Human SNP flanking
C 546	12.8	36.6	92	22	AAK24030	Human brain expres	C 619	12.6	36.0	51	22	AAE62759	Human SNP flanking
C 547	12.8	36.6	92	22	AAK50094	Human bone marrow	C 620	12.6	36.0	51	23	ABLO0199	Human D-SLAM 5' PC
C 548	12.8	36.6	92	22	AAI27180	Probe #17113 for g	C 621	12.6	36.0	51	24	AA25473	Human silent nonco
C 549	12.8	36.6	92	22	AAI56033	Probe #24719 used	C 622	12.6	36.0	51	24	AAI68013	Probe #10 used in
C 550	12.8	36.6	99	17	AAI39077	Partial T. verruco	C 623	12.6	36.0	51	24	AAI24697	ap2 mRNA specific
C 551	12.8	36.6	99	18	AAAT48765	Polyclonal anti-Fe	C 624	12.6	36.0	54	11	AAO05294	Probe #10, used in
C 552	12.6	36.0	20	21	AA230227	PCR primer G.-3 us	C 625	12.6	36.0	54	11	AAH99332	Dh region of 12 DN
C 553	12.6	36.0	21	21	AA505619	Methylenebisethydr	C 626	12.6	36.0	54	24	AAH99332	Oligonucleotide 4
C 554	12.6	36.0	21	22	AA205050	Human MTHFR DNA A1	C 627	12.6	36.0	56	18	AAV76939	Staphylococcus aur
C 555	12.6	36.0	23	22	AA514521	Human GSTT1 sequen	C 628	12.6	36.0	56	21	AAI11242	Human secreted pro
C 556	12.6	36.0	24	21	AA337230	Human DNA36958 rev	C 629	12.6	36.0	60	18	AAV77153	Staphylococcus aur
C 557	12.6	36.0	24	21	AA332522	Human male enhance	C 630	12.6	36.0	61	18	AAI57860	L-selectin family
C 558	12.6	36.0	24	22	AA543378	Primer #57 used in	C 631	12.6	36.0	63	12	AAE56814	VEGF receptor spec
C 559	12.6	36.0	24	22	AB190729	Capture oligonucle	C 632	12.6	36.0	71	18	AAV77639	Staphylococcus aur
C 560	12.6	36.0	24	24	AB190729	Capture oligonucle	C 633	12.6	36.0	71	18	AAE65191	Transforming growt
C 561	12.6	36.0	27	22	AAH39299	SNP specific SNPE	C 634	12.6	36.0	72	21	AA299550	Primer for catalyt
C 562	12.6	36.0	28	13	AAQ31105	Probe 74 to HCV-1	C 635	12.6	36.0	74	21	AA290046	Synthetic probe fo
C 563	12.6	36.0	29	21	AA661221	PCR primer 163 use	C 636	12.6	36.0	75	19	AAV31524	Human secreted pro
C 564	12.6	36.0	30	21	AA291885	PCR primer for str	C 637	12.6	36.0	76	21	AAV46575	Modified amyase g
C 565	12.6	36.0	31	16	AAQ93560	Human stromelysin	C 638	12.6	36.0	78	19	AAV19083	PCR primer used to
C 566	12.6	36.0	31	16	AAQ93561	Human stromelysin	C 639	12.6	36.0	80	17	AAV19083	Synthetic eglin ge
C 567	12.6	36.0	31	17	AAK63468	Human stromelysin	C 640	12.6	36.0	80	17	AAAT88625	VEGF nucleic acid
C 568	12.6	36.0	31	17	AAK63467	Human stromelysin	C 641	12.6	36.0	80	17	AAAT88625	VEGF nucleic acid
C 569	12.6	36.0	32	20	AAK63467	Human stromelysin	C 642	12.6	36.0	81	17	AAAT88625	BPI potentiating p
C 570	12.6	36.0	35	13	AAQ20605	PCR primer used to	C 643	12.6	36.0	82	21	AAAC23938	Human secreted pro
C 571	12.6	36.0	36	18	AAAT73037	Initiation region	C 644	12.6	36.0	83	16	AAAT26452	Human gene signatu
C 572	12.6	36.0	36	19	AAV54908	Mutagenic PCR prim	C 645	12.6	36.0	86	21	AAAC27450	Human secreted pro
C 573	12.6	36.0	36	20	AA223409	Primer used to int	C 646	12.6	36.0	88	22	ABA69648	Human foetal liver
C 574	12.6	36.0	36	20	AA223421	HPV16L1E7 fusion p	C 647	12.6	36.0	92	21	AAAC20889	Human secreted pro
C 575	12.6	36.0	36	20	AAK37586	Human papilloma v1	C 648	12.6	36.0	95	22	ABA20016	Human nervous syst
C 576	12.6	36.0	36	21	AA248194	HPV 16 L1 expressi	C 649	12.6	36.0	95	22	AAK70047	Human immune/haema
C 577	12.6	36.0	36	22	AAAD18957	PCR primer #15 to	C 650	12.6	36.0	95	22	AAK79968	Human immune/haema
C 578	12.6	36.0	36	22	AAE28082	Nascent protein de	C 651	12.6	36.0	95	22	AAK79969	Human immune/haema
C 579	12.6	36.0	38	17	AAAT10486	Human wild-type p5	C 652	12.6	36.0	95	22	AAK85214	Human immune/haema
C 580	12.6	36.0	38	18	AAAT88442	5' PCR primer 3 (s	C 653	12.6	36.0	98	16	AAO81918	Human immune/haema
C 581	12.6	36.0	38	21	AAAC73307	Single base extens	C 654	12.6	36.0	99	21	AAAC07982	Interferon-gamma b
C 582	12.6	36.0	40	20	AA224761	His tag linker oli	C 655	12.6	36.0	100	13	AAO31058	Human secreted pro
C 583	12.6	36.0	40	20	AAAD17982	A. fumigatus codon	C 656	12.6	36.0	100	20	AAZ06727	Insulin specific p
C 584	12.6	36.0	41	19	AAV51053	Maize polymorphic	C 657	12.6	36.0	100	20	AAK25515	Human interferon-a
C 585	12.6	36.0	41	22	AAE55872	Oligonucleotide #1	C 658	12.6	36.0	100	20	AAK25516	Human interferon-a
C 586	12.6	36.0	41	22	AAE55874	Murine IL-2 PCR pr	C 659	12.6	36.0	100	20	AAK25517	Human interferon-a
C 587	12.6	36.0	41	24	AAAD24571	Oligonucleotide #8	C 660	12.4	35.4	15	20	AAK31787	Transcript tag seq
C 588	12.6	36.0	43	20	AAH99929	Oligonucleotide 1	C 661	12.4	35.4	17	22	AAE30498	Human PAK5 Oligonu
C 589	12.6	36.0	43	20	AAZ24762	His tag linker oli	C 662	12.4	35.4	18	22	AAE38874	Human NOVNEUR DNA
C 590	12.6	36.0	44	16	AAO87784	Human auxiliary cy	C 663	12.4	35.4	19	21	AAZ70495	Human ballelic ma
C 591	12.6	36.0	44	17	AAAT48356	Sequence disclosed	C 664	12.4	35.4	20	20	AAK94299	PCR primer used to
C 592	12.6	36.0	44	17	AAAT26917	Human cytochrome p	C 665	12.4	35.4	20	21	AAAT71135	Single nucleotide
C 593	12.6	36.0	44	18	AAAT89937	CpTR exon 11 PCR p	C 666	12.4	35.4	20	21	AAAT71222	Single nucleotide

667	12.4	35.4	20	21	AAC71228	Single nucleotide	740	12.4	35.4	56	17	AAT26903	Human cytochrome P
C 668	12.4	35.4	21	17	AAT15458	Ceselin promoter-Co	741	12.4	35.4	58	17	AAT31636	Control template #
669	12.4	35.4	21	19	AAV20645	Human T-helper 2 s	C 742	12.4	35.4	59	16	AAT20783	Human gene signatu
670	12.4	35.4	21	19	AAV20540	Human T-helper 2 P	743	12.4	35.4	60	21	AA336837	Human dysferlin re
671	12.4	35.4	21	19	AAH62088	PCGF B hairpin/ham	744	12.4	35.4	60	21	AAH82928	Human dyferlin PC
672	12.4	35.4	23	19	AAV36060	Oligonucleotide W	745	12.4	35.4	62	22	AAH91516	PCR primer used to
673	12.4	35.4	24	17	AAT18342	Lee 14 promoter in	746	12.4	35.4	62	22	AAH500425	Human B7-3 5'-Rt P
674	12.4	35.4	24	17	AAH18452	Primer for DNA enc	747	12.4	35.4	63	9	AAH80984	pUC13 polylinker s
675	12.4	35.4	24	21	AAA39000	Human orphan recep	748	12.4	35.4	63	13	AAO20207	Mei cleavage site
676	12.4	35.4	24	21	AAZ50563	PCR primer-1 to am	C 749	12.4	35.4	64	19	AAV53687	Nucleotide sequenc
C 677	12.4	35.4	25	19	AAV20646	Human T-helper 2 s	C 750	12.4	35.4	64	19	AAV53688	Nucleotide sequenc
C 678	12.4	35.4	25	19	AAV20541	Human T-helper 2 P	C 751	12.4	35.4	64	20	AAH99459	Complementary olig
C 679	12.4	35.4	25	19	AAH64219	Human polliosis-a	C 752	12.4	35.4	64	20	AAH99460	Complementary olig
C 680	12.4	35.4	27	22	AAH57326	A. thaliana endo-x	C 753	12.4	35.4	64	20	AAV63744	Maize streak virus
681	12.4	35.4	30	20	AAH82477	Human CRT-1 DNA pr	754	12.4	35.4	66	16	AAO84333	Displacement trans
682	12.4	35.4	30	22	AAH21471	Soybean beta-actin	755	12.4	35.4	66	17	AAT31638	Primer DPA7 to gen
683	12.4	35.4	30	22	AAH84107	Yeast beta-type DN	756	12.4	35.4	69	4	AAH30111	Sequence of subseq
684	12.4	35.4	33	21	AAH12062	ETAV U3 enhancer r	757	12.4	35.4	72	7	AAH60980	Fragment BI is a P
C 685	12.4	35.4	33	22	AAH86628	Streptococcus pneu	C 758	12.4	35.4	75	17	AAT31620	Stem-loop amplifi
686	12.4	35.4	34	22	AAH81533	LTC4 receptor codi	C 759	12.4	35.4	75	17	AAT14375	Toxoplasma gondii
687	12.4	35.4	35	22	AAH84191	A. thaliana SVP ge	760	12.4	35.4	75	21	AAH18506	Human secreted pro
C 688	12.4	35.4	36	20	AAH78191	Selex procedure gr	761	12.4	35.4	76	17	AAT31619	Stem-loop amplifi
C 689	12.4	35.4	36	21	AAA35700	Permutin linker e	C 762	12.4	35.4	76	17	AAT04487	Single stranded st
690	12.4	35.4	36	21	AAH98816	PCR primer #1 for	763	12.4	35.4	76	21	AAH52802	WR33 heavy chain
C 691	12.4	35.4	36	21	AAH88102	3' U3 deletion mut	764	12.4	35.4	80	19	AAV49883	Murine cdc25b gene
C 692	12.4	35.4	36	21	AAH88131	Vector pTV PCR pri	C 765	12.4	35.4	80	20	AAZ30011	Oligonucleotide IF
C 693	12.4	35.4	37	11	AAO04499	Gastrin promoter.	766	12.4	35.4	80	20	AAH35327	Oligonucleotide IF
C 694	12.4	35.4	37	11	AAH30378	PCR primer used to	767	12.4	35.4	80	21	AAZ93022	Oligonucleotide us
695	12.4	35.4	37	22	AAH81547	LTC4 receptor codi	768	12.4	35.4	81	19	AAV44142	rhPDGF-B C-termin
696	12.4	35.4	38	18	AAT90036	Primer pMG3 for hu	769	12.4	35.4	82	22	AAH87272	Mouse growth hormo
697	12.4	35.4	40	20	AAH07210	Retroviral 3' U3-R	770	12.4	35.4	83	17	AAT39371	Human desmin gene
C 698	12.4	35.4	40	22	AAH17992	A. fumigatus codon	771	12.4	35.4	83	17	AAT39372	Human desmin gene
C 699	12.4	35.4	41	24	ABA92625	Human class II ami	772	12.4	35.4	83	17	AAT39373	Human desmin gene
C 700	12.4	35.4	41	24	ABA92625	Human class II ami	773	12.4	35.4	83	17	AAT39374	Human desmin gene
701	12.4	35.4	43	21	AAH00400	RT-PCR primer V13	774	12.4	35.4	83	17	AAT39375	Human desmin gene
702	12.4	35.4	45	14	AAO48422	Sense primer for p	775	12.4	35.4	83	17	AAT39376	Human desmin gene
703	12.4	35.4	45	16	AAT29937	Sense oligonucleot	776	12.4	35.4	83	17	AAT39377	Human desmin gene
704	12.4	35.4	45	16	AAT07594	RT-PCR primer/prob	777	12.4	35.4	83	17	AAT39378	Human desmin gene
705	12.4	35.4	45	16	AAT00652	Sense primer for t	778	12.4	35.4	83	17	AAT39379	Human desmin gene
706	12.4	35.4	46	15	AAO73417	PCR primer for HIV	779	12.4	35.4	83	17	AAT39380	Human desmin gene
C 707	12.4	35.4	47	17	AAT34834	Primer used in hum	780	12.4	35.4	83	17	AAT39381	Human desmin gene
708	12.4	35.4	47	21	AAZ65790	Human map-related	781	12.4	35.4	83	17	AAT39382	Human desmin gene
709	12.4	35.4	47	21	AAZ65881	Human map-related	C 782	12.4	35.4	84	20	AAZ30012	Oligonucleotide IF
C 710	12.4	35.4	47	21	AAZ67843	Human map-related	C 783	12.4	35.4	84	20	AAH76991	Chimeric oligonuci
C 711	12.4	35.4	47	21	AAZ69395	Human map-related	C 784	12.4	35.4	84	20	AAH76991	Chimeric oligonuci
712	12.4	35.4	47	22	AAH26376	Mollusc acetylchol	C 785	12.4	35.4	84	20	AAH76993	Chimeric oligonuci
C 713	12.4	35.4	48	19	AAV70097	Humanised HPE7A he	C 786	12.4	35.4	84	20	AAH76993	Chimeric oligonuci
714	12.4	35.4	48	20	AAH52510	PCR primer for in	C 787	12.4	35.4	84	20	AAH35328	Oligonucleotide us
C 715	12.4	35.4	48	21	AAA50605	CSFV envelope prot	C 788	12.4	35.4	84	21	AAZ93023	Oligonucleotide us
C 716	12.4	35.4	48	21	AAH72148	Humanised anti-Fas	C 789	12.4	35.4	86	17	AAT13959	Vacuolar-targetin
C 717	12.4	35.4	48	21	AAH1586	Humanised anti-Fas	C 790	12.4	35.4	86	18	AAT74021	Oligonucleotide en
718	12.4	35.4	49	17	AAH72710	Human PRO polypept	C 791	12.4	35.4	86	19	AAH16187	Oligonucleotide en
C 719	12.4	35.4	49	17	AAH34169	Human ob gene prim	C 792	12.4	35.4	89	19	AAH44141	Chimeric rhPDGF-B
C 720	12.4	35.4	50	18	AAV79414	Staphylococcus aur	C 793	12.4	35.4	90	20	AAH76987	Chimeric oligonuci
C 721	12.4	35.4	50	22	AAH28066	Human SNP oligonuc	C 794	12.4	35.4	90	20	AAH76987	Chimeric oligonuci
C 722	12.4	35.4	50	22	AAH30445	Human SNP oligonuc	C 795	12.4	35.4	90	20	AAH76989	Chimeric oligonuci
723	12.4	35.4	50	22	AAH32668	Human SNP oligonuc	C 796	12.4	35.4	90	20	AAH76989	Chimeric oligonuci
C 724	12.4	35.4	51	22	AAH76322	Human eph-like gen	C 797	12.4	35.4	91	20	AAH82658	Chimeric oligonuci
C 725	12.4	35.4	51	22	AAH27156	Human SNP oligonuc	C 798	12.4	35.4	91	22	AAH82658	Oligonucleotide us
726	12.4	35.4	51	22	AAH27343	Human SNP oligonuc	C 799	12.4	35.4	91	22	AAH57493	Probe #26179 used
C 727	12.4	35.4	51	22	AAH27778	Human SNP oligonuc	C 800	12.4	35.4	93	21	AAH09408	Human secreted pro
C 728	12.4	35.4	51	22	AAH30454	Human SNP oligonuc	C 801	12.4	35.4	95	22	AAH79248	Human alpha 2b int
C 729	12.4	35.4	51	22	AAH33316	Human SNP oligonuc	C 802	12.4	35.4	97	24	AAH12729	Coupled ligation a
C 730	12.4	35.4	51	22	AAH73561	Human silent SNP c	C 803	12.4	35.4	97	22	AAH17312	Coupled ligation a
C 731	12.4	35.4	51	22	AAH73805	Human silent SNP c	C 804	12.4	35.4	99	22	AAH50426	Human breast cell
C 732	12.4	35.4	51	22	AAH74090	Human silent SNP c	805	12.4	35.4	99	22	AAH68375	Human foetal liver
C 733	12.4	35.4	51	22	AAH74091	Human silent SNP c	806	12.4	35.4	99	22	AAH33733	Probe #15839 for g
C 734	12.4	35.4	51	22	AAH74414	Human silent SNP c	807	12.4	35.4	99	22	AAH16750	Human brain expres
C 735	12.4	35.4	51	22	AAH89586	Human collagen cod	808	12.4	35.4	99	22	AAH42521	Human bone marrow
C 736	12.4	35.4	52	21	AAH63315	Mycobacterium aviu	809	12.4	35.4	99	22	AAH23269	Probe #13202 for g
C 737	12.4	35.4	54	22	AAH32371	Xylanase related P	810	12.4	35.4	99	22	AAH48588	Probe #17274 used
C 738	12.4	35.4	56	16	AAH08770	Human auxillary cy	811	12.4	35.4	99	22	AAH08914	Probe #8905 used t
739	12.4	35.4	56	17	AAH48342	Primer for 0.9 kb	C 812	12.4	35.4	100	20	AAH86266	Human single nucle

813	12.2	34.9	17	20	AA17275	Aryl hydrocarbon n	886	12.2	34.9	36	23	AA596469	HPV16 E7 mutagenic
C 814	12.2	34.9	17	22	AAH94711	Human Chk1 ribozym	887	12.2	34.9	37	22	AA67239	Fibrosis modulator
815	12.2	34.9	20	18	AA92761	Primer #2 for live	C 888	12.2	34.9	39	18	AA77349	PCR primer 2 used
816	12.2	34.9	20	19	AA52758	Liver fatty acid b	C 889	12.2	34.9	39	19	AAV2905	TBV25-Fts28D fusio
C 817	12.2	34.9	20	19	AA96041	Primer for chicken	890	12.2	34.9	39	19	AAV29085	TBV25-Fts28B fusio
818	12.2	34.9	20	20	AA205178	PCR primer used to	891	12.2	34.9	39	19	AAV29085	TBV25-Fts28C fusio
819	12.2	34.9	20	21	AA47631	Intronc primer (7	C 892	12.2	34.9	39	21	AA502099	PCR primer # 8 use
C 820	12.2	34.9	20	21	AA40881	Murine TNFalpha an	C 893	12.2	34.9	40	14	AA050877	HSV2 primer. Synt
C 821	12.2	34.9	20	21	AA414042	Human liver glycog	C 894	12.2	34.9	40	16	AA087601	Primer to PCR ampl
C 822	12.2	34.9	20	21	AA409921	Primer 2 for human	C 895	12.2	34.9	40	16	AA085338	PCR primer fragmen
C 823	12.2	34.9	20	22	AA506996	Primer BETH-R used	896	12.2	34.9	40	21	AA000410	Human ubiquitin RT
824	12.2	34.9	21	23	AA96015	Human gene single	897	12.2	34.9	41	16	AA075067	Human cyclin A DNA
C 825	12.2	34.9	21	23	AAH88958	Human polymorphic	898	12.2	34.9	41	20	AA16198	Serine protease in
C 826	12.2	34.9	22	21	AA99831	Human complement 9	899	12.2	34.9	41	20	AA16208	Serine protease in
C 827	12.2	34.9	22	21	AA36912	Human dysferlin ex	900	12.2	34.9	41	21	AA697556	Primer used in pro
C 828	12.2	34.9	22	21	AA11457	Human dysferlin PC	901	12.2	34.9	41	21	AA697556	Primer used in pro
C 829	12.2	34.9	22	22	AA632596	Human complement 9	902	12.2	34.9	41	22	AA167498	Serine protease in
C 830	12.2	34.9	22	22	AA629542	Human complement 9	903	12.2	34.9	41	22	AA167508	Serine protease in
C 831	12.2	34.9	23	17	AA18135	Streptococcus muta	904	12.2	34.9	42	16	AA108214	Amplification prim
832	12.2	34.9	23	20	AA990033	Human monoclonal a	905	12.2	34.9	47	10	AAAN0999	Fragments 3 & 4 of
C 833	12.2	34.9	23	21	AA990088	Lambda gt10cDNA PC	C 906	12.2	34.9	47	17	AA132280	Primer used in con
834	12.2	34.9	23	21	AA13942	Human PTHrP monocl	C 907	12.2	34.9	47	21	AA266924	Human map-related
C 835	12.2	34.9	23	22	AA015242	23 mer oligo probe	C 908	12.2	34.9	47	21	AA267305	Human map-related
C 836	12.2	34.9	24	22	AAH28664	Human Interleukin-	C 909	12.2	34.9	47	21	AA267606	Human map-related
C 837	12.2	34.9	25	9	AAH82014	Anti-sense PCR pri	C 910	12.2	34.9	47	21	AA268094	Human map-related
C 838	12.2	34.9	25	13	AA020981	Human COL1A1 PCR p	C 911	12.2	34.9	47	21	AA268605	Human map-related
C 839	12.2	34.9	25	13	AA020981	Human COL1A1 PCR p	C 912	12.2	34.9	47	21	AA269337	Human map-related
840	12.2	34.9	25	15	AA500923	Beetle luciferase	C 913	12.2	34.9	48	5	AAAN0205	Sequence of multilf
C 841	12.2	34.9	25	15	AA061525	CD3 delta enhancer	914	12.2	34.9	48	7	AAAN0908	Sequence of multilf
842	12.2	34.9	26	19	AA067086	Mouse CD3-delta en	915	12.2	34.9	49	18	AA180441	Sequence of multilf
C 843	12.2	34.9	26	19	AAV45379	Mouse CD3-delta en	916	12.2	34.9	50	21	AA11037	Sequence of multilf
C 844	12.2	34.9	26	19	AAV32728	Human GST-pi gene	C 917	12.2	34.9	50	22	AA129986	Sequence of multilf
845	12.2	34.9	26	19	AAV17188	Information carryi	918	12.2	34.9	51	21	AA177161	Sequence of multilf
C 846	12.2	34.9	27	19	AA95477	Human c-fos hamme	919	12.2	34.9	51	21	AA248831	Sequence of multilf
C 847	12.2	34.9	27	20	AA21274	Lactococcus lactis	C 920	12.2	34.9	51	21	AA248831	Sequence of multilf
C 848	12.2	34.9	27	20	AA21276	Lactococcus lactis	C 921	12.2	34.9	51	22	AA248831	Sequence of multilf
C 849	12.2	34.9	27	20	AA21277	Lactococcus lactis	C 922	12.2	34.9	51	22	AA248831	Sequence of multilf
C 850	12.2	34.9	27	20	AA21282	Lactococcus lactis	C 923	12.2	34.9	51	22	AA248831	Sequence of multilf
C 851	12.2	34.9	27	20	AA21282	Lactococcus lactis	C 924	12.2	34.9	51	22	AA248831	Sequence of multilf
C 852	12.2	34.9	27	24	AA25448	Saccharomyces cere	925	12.2	34.9	51	22	AA248831	Sequence of multilf
C 853	12.2	34.9	29	21	AA25448	HPV 16 gene LCR re	926	12.2	34.9	51	22	AA248831	Sequence of multilf
C 854	12.2	34.9	29	21	AA25448	Rhesus monkey mela	927	12.2	34.9	51	22	AA248831	Sequence of multilf
C 855	12.2	34.9	29	21	AA25448	Neisseria meningit	928	12.2	34.9	51	22	AA248831	Sequence of multilf
C 856	12.2	34.9	30	12	AAV02925	5' primer (88-412)	C 929	12.2	34.9	51	22	AA248831	Sequence of multilf
C 857	12.2	34.9	30	19	AAV21270	Human GAPDH Intron	C 930	12.2	34.9	51	22	AA248831	Sequence of multilf
C 858	12.2	34.9	30	20	AAV83821	Tissue plasminogen	C 931	12.2	34.9	51	22	AA248831	Sequence of multilf
859	12.2	34.9	30	21	AA73215	PCR primer used to	932	12.2	34.9	51	22	AA248831	Sequence of multilf
C 860	12.2	34.9	30	21	AA73215	HIV-1 gag INS gene	933	12.2	34.9	51	22	AA248831	Sequence of multilf
C 861	12.2	34.9	30	21	AA73215	PCR primer-2 for g	934	12.2	34.9	51	22	AA248831	Sequence of multilf
C 862	12.2	34.9	30	22	AAH44863	PCR primer PH785 u	C 935	12.2	34.9	51	23	AAH44863	Sequence of multilf
C 863	12.2	34.9	30	22	AAH44863	Human GAPDH Intron	C 936	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 864	12.2	34.9	30	22	AAH44863	PCR primer used to	937	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 865	12.2	34.9	31	22	AA39066	Human genomic DNA	938	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 866	12.2	34.9	31	22	AA39066	Human single nucle	C 939	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 867	12.2	34.9	31	22	AA39066	Human single nucle	C 940	12.2	34.9	52	22	AAH44863	Sequence of multilf
868	12.2	34.9	31	22	AA39066	Human single nucle	941	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 869	12.2	34.9	31	24	AA39066	Human single nucle	942	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 870	12.2	34.9	31	24	AA39066	Mouse zmsel (musm)	943	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 871	12.2	34.9	32	22	AA02726	Human ABC2 transpo	C 944	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 872	12.2	34.9	32	22	AA02726	Rhodococcus scra	C 945	12.2	34.9	52	22	AAH44863	Sequence of multilf
873	12.2	34.9	33	21	AA87107	Human TRAP220 muta	C 946	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 874	12.2	34.9	33	21	AA87107	Human TRAP220 muta	C 947	12.2	34.9	52	22	AAH44863	Sequence of multilf
C 875	12.2	34.9	33	24	AA05079	Oligo 14F, to cons	C 948	12.2	34.9	52	24	AA05079	Sequence of multilf
C 876	12.2	34.9	34	18	AA788883	Human zinc finger	949	12.2	34.9	53	13	AA020345	Sequence of multilf
877	12.2	34.9	34	19	AA788883	Primer NI for Fas	C 950	12.2	34.9	53	13	AA020345	Sequence of multilf
C 878	12.2	34.9	34	19	AA788883	Human Fas antigen	951	12.2	34.9	53	13	AA020345	Sequence of multilf
C 879	12.2	34.9	34	21	AA788883	PCR primer used to	952	12.2	34.9	53	13	AA020345	Sequence of multilf
880	12.2	34.9	34	21	AA788883	E. coli atoc gene	953	12.2	34.9	53	13	AA020345	Sequence of multilf
C 881	12.2	34.9	34	21	AA788883	Human Fas extracel	C 954	12.2	34.9	53	13	AA020345	Sequence of multilf
882	12.2	34.9	34	24	AA788883	Human Fas antigen	955	12.2	34.9	53	13	AA020345	Sequence of multilf
C 883	12.2	34.9	36	22	AA788883	Viral promoter fra	C 956	12.2	34.9	53	13	AA020345	Sequence of multilf
C 884	12.2	34.9	36	22	AA788883	Primer used to pro	957	12.2	34.9	53	13	AA020345	Sequence of multilf
C 885	12.2	34.9	36	23	AA788883	HPV16 E7 mutagenic	C 958	12.2	34.9	53	13	AA020345	Sequence of multilf

```

959 12.2 34.9 71 18 AAT57859 L-selectin family
c 960 12.2 34.9 71 18 AAT57830 L-selectin family
961 12.2 34.9 72 22 AAT78935 cDNA encoding rat
962 12.2 34.9 73 16 AAQ99756 Pseudomonas ergino
c 963 12.2 34.9 73 17 AAT71363 Red blood cell gho
964 12.2 34.9 74 11 AAQ03841 Synthetic sequence
965 12.2 34.9 74 11 AAQ03840 Synthetic sequence
966 12.2 34.9 74 11 AAQ03839 Synthetic sequence
967 12.2 34.9 74 22 AAS43691 Corneodesmosin sin
968 12.2 34.9 74 22 AAS43692 Corneodesmosin sin
c 969 12.2 34.9 75 13 AAQ03086 Primer 312-60. Sy
970 12.2 34.9 77 18 AAT84612 Synthetic tac prom
c 971 12.2 34.9 77 18 AAT79108 HIV-1 nucleocapsid
c 972 12.2 34.9 77 18 AAT79108 RNA ligand to HIV-
c 973 12.2 34.9 77 22 ABA70048 Human foetal liver
c 974 12.2 34.9 77 22 AAK18257 Human brain expres
c 975 12.2 34.9 77 22 AAK44153 Human bone marrow
c 976 12.2 34.9 77 22 AAK44538 Human bone marrow
c 977 12.2 34.9 77 22 AAI50161 Probe #18847 used
c 978 12.2 34.9 77 22 AAI50526 Probe #19212 used
c 979 12.2 34.9 78 13 AAQ23534 CMV35S promoter B
980 12.2 34.9 79 22 ABA47271 Human breast cell
981 12.2 34.9 79 22 ABA65156 Human foetal liver
982 12.2 34.9 79 22 ABA33258 Probe #10724 for g
983 12.2 34.9 79 22 AAK13575 Human brain expres
984 12.2 34.9 79 22 AAK33114 Human bone marrow
985 12.2 34.9 79 22 AAI20127 Probe #10060 for g
986 12.2 34.9 79 22 AAI45327 Probe #14013 used
987 12.2 34.9 80 9 AAN80462 Expression-control
988 12.2 34.9 81 12 AAQ13139 Hybrid promoter
989 12.2 34.9 81 12 AAQ14475 Hybrid of T3 phage
990 12.2 34.9 81 16 AAT06268 HIV-1 reverse tran
991 12.2 34.9 81 16 AAT06269 HIV-1 reverse tran
992 12.2 34.9 82 20 AAX32349 Artificial NS4 mos
c 993 12.2 34.9 82 24 AAD22604 BVDV CP7 cDNA muta
994 12.2 34.9 83 22 AAH28258 Oligonucleotide en
995 12.2 34.9 85 4 AAN30119 Sequence of the tr
996 12.2 34.9 85 22 AAG89215 Human brain T calc
997 12.2 34.9 86 22 ABA50507 Human breast cell
998 12.2 34.9 86 22 ABA68458 Human foetal liver
999 12.2 34.9 86 22 AAI6829 Human brain expres
1000 12.2 34.9 86 22 AAK42600 Human bone marrow

```

ALIGNMENTS

```

RESULT 1
AAN60796/c
ID AAN60796 standard; DNA; 46 BP.
XX
XX AAN60796;
AC
XX 01-JUL-1991 (first entry)
DT
XX
XX Sequence of probe substantially homologous with the DOB gene of the
DE HLA.
DE
XX
XX Probe; hybridisation; diabetes; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..19
FT misc-feature /*tag= a
FT /*note= "also claimed as a probe"
XX
XX WO8607464-A.
XX
XX 18-DEC-1986.
XX
XX 13-JUN-1986; 86WO-0001292.
XX

```

```

PR 14-JUN-1985; 85US-0745321.
XX
XX (GENE-) GENETIC SYST CORP.
XX
XX Nepom GT, Nepom BS, Nelson RA;
XX
XX WPI; 1986-34665/52.
XX
XX Detection of alleles associated with increased risk of diabetes -
PT using two different specified monoclonal antibodies
XX
XX Claim 15; Page 19; 20pp; English.
XX
XX The probes are used in a method for identifying individuals at
CC increased risk of diabetes. The probe can be labelled with a
CC radioisotope or an enzyme.
XX
SQ Sequence 46 BP; 12 A; 19 C; 10 G; 5 T; 0 other;

```

```

Query Match 52.0%; Score 18.2; DB 7; Length 46;
Best Local Similarity 74.2%; Pred. No. 2.4e+02;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 3 tgctagaatgggagatggggtcactctggac 33
DB 34 TGTCTCGATGGGAGATGTCATCTGTGGC 4

```

RESULT 2

```

AAT73976
ID AAT73976 standard; DNA; 51 BP.
XX
XX AAT73976;
AC
XX 09-NOV-2001 (first entry)
DT
XX
XX Human silent SNP containing nucleic acid SEQ:917.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US32758.
XX
XX 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
XX
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
XX Claim 1; Page 334; 2653pp; English.
XX
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations

```


CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patient's own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 51 BP; 6 A; 20 C; 19 G; 6 T; 0 other;

Query Match 50.3%; Score 17.6; DB 22; Length 51;
Best Local Similarity 71.9%; Pred. No. 4.3e+02;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 3 tgtctagaatgggagtggtcactctgacc 34
||||| ||||| ||||| ||||| |||||
Db 12 tgcttatgtctgggacggcgctcagttcc 43

RESULT 3
AA173978
ID AA173978 standard; DNA: 51 BP.

AC AA173978:

DT 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:919.

DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US32758.

PR 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
therapy -

PS Claim 1; Page 334; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA53114 to AA53129 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patient's own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids

CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 51 BP; 6 A; 22 C; 17 G; 6 T; 0 other;

Query Match 50.3%; Score 17.6; DB 22; Length 51;
Best Local Similarity 71.9%; Pred. No. 4.3e+02;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 3 tgtctagaatgggagtggtcactctgacc 34
||||| ||||| ||||| ||||| |||||
Db 10 tgcttatgtctgggacggcgctcagttcc 41

RESULT 4
AAV39899/c
ID AAV39899 standard; DNA: 38 BP.

AC AAV39899:

DT 02-OCT-1998 (first entry)

XX Streptococcus pneumoniae ORF cloning primer SEQ ID NO:382.

DE Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;

KW detection; pneumonia; otitis media; meningitis; cloning primer; ss.

XX Synthetic.

OS Streptococcus pneumoniae.

XX WO9818930-A2.

PD 07-MAY-1998.

PF 30-OCT-1997; 97WO-US19422.

PR 31-OCT-1996; 96US-0029960.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Choi GH, Hromocky J A, Johnson LS, Kunsch CA;

DR WPI; 1998-272224/24.

PT Nucleic acid encoding antigenic peptide(s) from Streptococcus

PT pneumoniae - or their epitope-containing fragments, useful in

PT protective or therapeutic vaccines, and for diagnosis

PS Example 1; Page 108; 118pp; English.

XX The present sequence represents a cloning primer used in an example from
CC the present invention which describes proteins from Streptococcus
CC pneumoniae. Nucleic acid sequence encoding Streptococcus pneumoniae
CC proteins can be useful in vaccines for inducing protective antibodies
CC against Streptococcus pneumoniae, for treatment or prevention of
CC infection e.g. pneumonia, otitis media or meningitis. Probes based on
CC the nucleic acids are used to detect Streptococcus infection (by usual
CC hybridisation or amplification methods), also for isolating

CC Streptococcus genes or their allelic variants. The proteins can be used

CC similarly to detect specific antibodies in standard immunoassays,

CC especially for diagnosing or monitoring infections. Antibodies which

CC bind the proteins are used to detect corresponding antigens, to purify
CC the proteins and for passive immunisation (optionally coupled to a
CC toxin). Vaccines are administered, e.g. by injection, orally or through
CC the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.

CC The cloning primers used in the present invention are given in AAV27437
CC to AAV27562 and AAV39870 to AAV39969.

XX OS Synthetic.
XX PN WO9605315-A2.
XX PD 22-FEB-1996.
XX PF 15-AUG-1995; 95MO-US10398.
XX PR 15-AUG-1994; 94US-0290665.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI (USSH) US SEC DEPT HEALTH.
XX PI Bukh J, Miller RH, Purcell RH;
XX WPI: 1996-139709/14.
XX DR
XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins -
XX PT used to determine HCV genotype and as vaccines against HCV infection
XX PS Disclosure; Page 229; 340pp; English.
XX CC AAT16662-T16688 are primers derived from a set of 51 different HCV
XX CC EI (envelope-1) gene isolates that are useful for detecting the
XX CC presence of HCV in a sample, the primers are genotype-specific and
XX CC so are also useful for genotyping HCV CDNAs. Proteins encoded by HCV
XX CC EI CDNAs can be used in vaccines for immunising against HCV infection.
XX CC The proteins may also be used to detect antibodies against HCV in
XX CC serum, saliva, lymphocytes or other mononuclear cells. The antibodies
XX CC may be used in the prevention of HCV infection.
XX SQ Sequence 42 BP; 7 A; 13 C; 13 G; 9 T; 0 other;

Query Match 48.0%; Score 16.8; DB 17; Length 42;
Best Local Similarity 75.0%; Pred. No. 8.9e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 catgtctagaatggagtggtgctac 28
||||| ||||| ||||| |||||
Db 30 CATGTCGAGAAAGCGCTGTGGGACCCTC 3

RESULT 8
AAL33984/c
ID AAL33984 standard; DNA: 50 BP.
XX AC AAL33984;
XX

DT 24-JAN-2002 (first entry)
XX

DE Human SNP oligonucleotide #7192.
XX

XX Immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; colony stimulating factor;
XX complement related protein; cytochrome; kinase; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.
XX

OS Homo sapiens.
XX

PN WO200147944-A2.
XX

PD 05-JUL-2001.
XX

PF 28-DEC-2000; 2000MO-US35498.
XX

PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX

XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach M;
XX DR WPI: 2001-465210/50.
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX cancer, autoimmune diseases and infections -
XX PS Claim 1; Page 3450; 4143pp; English.
XX CC The present invention relates to oligonucleotides encoding polymorphic
XX CC variants of proteins related to amylases, amyloid proteins, angiotensin,
XX CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX CC histones, kinases, colony stimulating factors, complement related
XX CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX CC G-protein coupled receptors and thioesterases. The present sequence is
XX CC one such oligonucleotide. The oligonucleotides and the peptides encoded
XX CC by them may be used in the prevention, diagnosis and treatment of
XX CC diseases associated with inappropriate expression of the proteins listed
XX CC above. Disorders that may be prevented, diagnosed and/or treated include
XX CC multifactorial diseases with a genetic component, such as autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX CC leukaemia), diseases of the nervous system and an infection of pathogenic
XX CC organisms.
XX SQ Sequence 50 BP; 11 A; 16 C; 10 G; 13 T; 0 other;

Query Match 46.9%; Score 16.4; DB 22; Length 50;
Best Local Similarity 76.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 7 tagaatggagtggtggtgctctga 32
||||| ||||| ||||| |||||
Db 40 TAGACTGGGGCTCGGCTCGCTCTGAA 15

RESULT 9
AAF26235/c
ID AAF26235 standard; DNA: 36 BP.
XX AC AAF26235;
XX

DT 02-MAY-2001 (first entry)
XX

DE B. megaterium cytochrome P450 monooxygenase BM-3 associated primer B1.
XX

XX Cytochrome P450 monooxygenase: BM-3; electron donor system; bioreactor;
XX electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase;
XX primer; ss.
XX

OS Bacillus megaterium.
XX

PN WO200107573-A1.
XX

PD 01-FEB-2001.
XX

PF 27-JUL-2000; 2000MO-EP07251.
XX

PR 27-JUL-1999; 99DE-1035115.
XX

PR 10-MAR-2000; 2000DE-1011723.
XX

PA (BADI) BASF AG.
XX

PI Hauer B, Schmid RD, Schwaneberg U;
XX
XX WPI: 2001-159709/16.
XX


```
PT a mediator which enables the electron transfer -
XX
PS Example 2; Page 75; 94pp; German.
XX
CC This invention describes a novel electron donor system (M1) that
CC transfers electrons to an enzyme with redox properties comprising an
CC inorganic, not electrode-bound, electron sink and a mediator which enable
CC the electron transfer. The invention also describes (1) transferring (M2)
CC oxygen to a hydrocarbon containing hydrogen donor molecule, where the
CC hydrogen donor molecule is in a reaction medium comprising the oxygen
CC transferring enzyme and (M1) in the presence of oxygen and incubating
CC under suitable reaction conditions; (2) the enzymatic production (M3) of
CC terminally or subterminally hydroxylated (position omega-1 to omega-4)
CC fatty acids comprising: (1) mixing a hydroxylatable fatty acid or fatty
CC acid derivative in the presence of (M1) and cytochrome P450
CC monooxygenase; and (11) isolating the hydroxylated product; (3) a
CC bioreactor useful for the production of omega-hydroxylated fatty acids as
CC described in (2); and (4) detecting (M4) fatty acid-monooxygenases
CC comprising: (1) contacting the analyte with a omega-hydroxylatable fatty
CC acid or a derivative comprising a terminal chromophore or fluorescent
CC label in (M1); and (11) qualitatively or quantitatively detecting the
CC signal. The invention is useful for the production of omega-hydroxylated
CC fatty acids and the detection of fatty acid monooxygenases. The
CC invention provides an alternative electron donor system of enzymes with
CC redox properties that is cheaper and more efficient, where the enzyme
CC comprises cytochrome 450.
XX
SQ Sequence 36 BP; 15 A; 6 C; 9 G; 6 T; 0 other:

Query Match          46.3%; Score 16.2; DB 22; Length 36;
Best Local Similarity 72.4%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 catgtctagaatgggagtggtcactct 29
   ||| ||| ||| ||| ||| ||| ||| |||
Db 34 CATTTCTTTAATGTCATGGATCCCTCT 6

RESULT 12
AAF26262/C
ID AAF26262 standard; DNA; 36 BP.
AC
AC AAF26262;
XX
DF 02-MAY-2001 (first entry)
XX
DE B. megaterium BM-3 associated primer H1.
XX
KW Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor;
KW electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase;
KW primer; ss.
XX
OS Bacillus megaterium.
XX
PN WO200107573-A1.
XX
PD 01-FEB-2001.
XX
PF 27-JUL-2000; 2000WO-EP07251.
XX
PR 27-JUL-1999; 99DE-1035115.
XX
PR 10-MAR-2000; 2000DE-1011723.
XX
PA (BADT ) BASF AG.
XX
PI Hauser B, Schmid RD, Schwaneberg U;
XX
DR WPI; 2001-159709/16.
XX
PT Novel electron donor system useful for the production of
PT omega-hydroxylated fatty acids comprises an inorganic electron sink and
PT a mediator which enables the electron transfer -
XX
```

```
XX
PS Example 2; Page 76; 94pp; German.
XX
CC This invention describes a novel electron donor system (M1) that
CC transfers electrons to an enzyme with redox properties comprising an
CC inorganic, not electrode-bound, electron sink and a mediator which enable
CC the electron transfer. The invention also describes (1) transferring (M2)
CC oxygen to a hydrocarbon containing hydrogen donor molecule, where the
CC hydrogen donor molecule is in a reaction medium comprising the oxygen
CC transferring enzyme and (M1) in the presence of oxygen and incubating
CC under suitable reaction conditions; (2) the enzymatic production (M3) of
CC terminally or subterminally hydroxylated (position omega-1 to omega-4)
CC fatty acids comprising: (1) mixing a hydroxylatable fatty acid or fatty
CC acid derivative in the presence of (M1) and cytochrome P450
CC monooxygenase; and (11) isolating the hydroxylated product; (3) a
CC bioreactor useful for the production of omega-hydroxylated fatty acids as
CC described in (2); and (4) detecting (M4) fatty acid-monooxygenases
CC comprising: (1) contacting the analyte with a omega-hydroxylatable fatty
CC acid or a derivative comprising a terminal chromophore or fluorescent
CC label in (M1); and (11) qualitatively or quantitatively detecting the
CC signal. The invention is useful for the production of omega-hydroxylated
CC fatty acids and the detection of fatty acid monooxygenases. The
CC invention provides an alternative electron donor system of enzymes with
CC redox properties that is cheaper and more efficient, where the enzyme
CC comprises cytochrome 450.
XX
SQ Sequence 36 BP; 15 A; 6 C; 9 G; 6 T; 0 other:

Query Match          46.3%; Score 16.2; DB 22; Length 36;
Best Local Similarity 72.4%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 catgtctagaatgggagtggtcactct 29
   ||| ||| ||| ||| ||| ||| ||| |||
Db 34 CATTTCTTTAATGTCATGGATCCCTCT 6

RESULT 13
AAF83314
ID AAF83314 standard; DNA; 36 BP.
AC
AC AAF83314;
XX
DF 09-JUL-2001 (first entry)
XX
DE Human neuropilin-1 (NP-1) DNA amplifying sense primer BUL-265.
XX
KW Receptor protein; vascular endothelial growth factor receptor-2; NP-1;
KW VEGFR-2; neuropilin-1; co-receptor; human; angiogenic; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200131346-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US29579.
XX
PR 28-OCT-1999; 99US-0162367.
XX
PA (PROCTER & GAMBLE CO.
XX
PI Rosenbaum JS, Whitaker GB, Limberg BJ;
XX
DR WPI; 2001-308686/32.
XX
PT Determining compounds which bind to a complex comprising vascular
PT endothelial growth factor receptor-2 and Neuropilin-1 to provide
PT superior pro- and anti-angiogenic agents -
XX
PS Example 1; Fig 3; 82pp; English.
XX
```


XX Sequence 51 BP; 6 A; 23 C; 16 G; 6 T; 0 other;

Query Match 45.7%; Score 16; DB 22; Length 51;
 Best Local Similarity 68.8%; Pred. No. 2e+03;
 Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 tgctcagaatgggagtggtcactctggacc 34
 |||||
 Db 10 tgcttatgctggygacggygcgcgtcaggcc 41

Search completed: June 22, 2002, 05:40:15
 Job time: 5090 sec

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 05:33:31 ; Search time 98.05 Seconds
(Without alignments)
87.682 Million cell updates/sec

Title: US-09-927-267-13

Perfect score: 35

Sequence: 1 catgctagaatgggagtcactctgacact 35

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Searched: 383533 seqs, 122816752 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	17.2	49.1	38	3	US-08-961-083-382
C 3	16.8	48.0	42	1	US-08-086-4288-124
C 4	16.8	48.0	42	2	US-08-468-570-124
C 5	16.8	48.0	42	2	US-08-290-665A-228
C 6	16.8	48.0	42	5	PCT-US95-10398-228
C 7	15.8	45.1	75	1	US-08-482-111-61
C 8	15.4	44.0	81	1	US-08-238-863-78
C 9	15.4	44.0	81	1	US-08-443-407-78
C 10	15.4	44.0	81	5	PCT-US95-05600-222
C 11	15.4	44.0	100	4	US-08-954-395A-28
C 12	15.4	44.0	32	1	US-08-221-817-8
C 13	15.4	42.9	32	1	US-08-454-439-8
C 14	15.4	42.9	32	5	PCT-US94-10487-8
C 15	14.6	41.7	21	1	US-07-665-960A-10
C 16	14.6	41.7	21	1	US-08-106-802-10
C 17	14.6	41.7	21	2	US-08-703-136-10
C 18	14.6	41.7	51	2	US-08-883-795A-10
C 19	14.6	41.7	51	2	US-08-883-795A-26
C 20	14.4	41.1	39	1	US-08-121-202-16
C 21	14.2	40.6	26	4	US-09-268-163-16
C 22	14.2	40.6	33	6	5196305-1
C 23	14.2	40.6	83	4	US-08-729-601A-25
C 24	14.2	40.6	29	2	US-08-664-872-14
C 25	14.2	40.0	29	4	US-09-019-973-16
C 26	14.2	40.0	73	4	US-09-564-805-13
C 27	14.2	40.0	79	1	US-08-384-708A-212

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30	14	40.0	79	5	PCT-US96-09452-10	Sequence 10, App1
C 31	14	40.0	86	1	US-08-447-169A-177	Sequence 177, App
C 32	14	40.0	96	1	US-08-253-877C-16	Sequence 16, App1
C 33	14	40.0	96	2	US-08-452-164A-16	Sequence 16, App1
C 34	14	40.0	96	3	US-08-603-024-15	Sequence 15, App1
C 35	13.8	39.4	30	2	US-08-829-876-20	Sequence 20, App1
C 36	13.8	39.4	39	3	US-08-643-704A-37	Sequence 37, App1
C 37	13.8	39.4	50	1	US-08-171-389-532	Sequence 532, App
C 38	13.8	39.4	50	1	US-08-123-936-532	Sequence 532, App
C 39	13.8	39.4	50	2	US-08-475-228A-532	Sequence 532, App
C 40	13.8	39.4	50	3	US-08-482-080A-532	Sequence 532, App
C 41	13.8	39.4	50	5	PCT-US93-12388-532	Sequence 532, App
C 42	13.8	39.4	60	3	US-08-643-704A-11	Sequence 11, App1
C 43	13.8	39.4	81	1	US-08-238-863-90	Sequence 90, App1
C 44	13.8	39.4	81	1	US-08-443-407-90	Sequence 90, App1
C 45	13.8	39.4	81	5	PCT-US95-05600-234	Sequence 234, App1
C 46	13.8	39.4	100	4	US-08-954-395A-24	Sequence 24, App1
C 47	13.6	38.9	22	2	US-08-451-822A-6	Sequence 6, App1
C 48	13.6	38.9	22	4	US-08-323-430-6	Sequence 6, App1
C 49	13.6	38.9	31	3	US-09-032-894-109	Sequence 109, App
C 50	13.6	38.9	31	3	US-09-032-894-111	Sequence 111, App
C 51	13.6	38.9	31	4	US-09-031-626-109	Sequence 109, App
C 52	13.6	38.9	31	4	US-09-031-626-111	Sequence 111, App
C 53	13.6	38.9	32	1	US-07-990-965-2	Sequence 2, App1
C 54	13.6	38.9	40	4	US-09-262-773-128	Sequence 128, App
C 55	13.6	38.9	42	3	US-08-874-825-42	Sequence 42, App1
C 56	13.6	38.9	42	3	US-08-663-824-42	Sequence 42, App1
C 57	13.6	38.9	48	5	PCT-US94-07779-2	Sequence 2, App1
C 58	13.6	38.9	61	4	US-08-952-793-377	Sequence 377, App
C 59	13.6	38.9	61	5	PCT-US96-09455A-377	Sequence 377, App
C 60	13.4	38.3	26	4	US-09-147-915-11	Sequence 11, App1
C 61	13.4	38.3	28	4	US-09-324-867-42	Sequence 42, App1
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C 74	13.2	37.7	28	1	US-07-601-094-17	Sequence 17, App1
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113	13.2	37.7	84	2	US-08-807-861A-9	Sequence 9, Appl	186	12.8	36.6	60	3	US-08-911-884-65	Sequence 65, Appl
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115	13.2	37.7	84	2	US-08-470-868A-9	Sequence 9, Appl	188	12.8	36.6	60	3	US-08-911-884-68	Sequence 68, Appl
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130	13	37.1	36	5	PCT-US92-09487-83	Sequence 83, Appl	203	12.6	36.0	20	2	US-08-406-057-12	Sequence 12, Appl
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132	13	37.1	41	1	US-08-399-696-32	Sequence 32, Appl	205	12.6	36.0	21	5	PCT-US96-00996-21	Sequence 21, Appl
133	13	37.1	46	1	US-07-885-689A-17	Sequence 17, Appl	206	12.6	36.0	24	4	US-09-011-922A-12	Sequence 12, Appl
134	13	37.1	48	1	US-08-436-717-83	Sequence 7, Appl	207	12.6	36.0	28	3	US-08-441-971-74	Sequence 74, Appl
135	13	37.1	48	1	US-08-137-117D-83	Sequence 83, Appl	208	12.6	36.0	28	4	US-08-221-653-74	Sequence 74, Appl
136	13	37.1	48	1	US-08-436-717-83	Sequence 83, Appl	209	12.6	36.0	28	4	US-08-442-144A-74	Sequence 74, Appl
137	13	37.1	48	2	US-08-241-664B-7	Sequence 7, Appl	210	12.6	36.0	28	4	US-08-441-970-74	Sequence 74, Appl
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139	13	37.1	48	4	US-09-503-222-8	Sequence 8, Appl	212	12.6	36.0	31	1	US-08-390-850-100	Sequence 100, Appl
140	13	37.1	54	2	US-08-448-418-23	Sequence 23, Appl	213	12.6	36.0	31	1	US-08-435-634-99	Sequence 99, Appl
141	13	37.1	56	1	US-08-263-020-8	Sequence 8, Appl	214	12.6	36.0	31	1	US-08-435-634-100	Sequence 100, App
142	13	37.1	56	3	US-08-973-965-41	Sequence 41, Appl	215	12.6	36.0	35	5	PCT-US91-04492-1	Sequence 1, Appl
143	13	37.1	60	2	US-08-707-237A-30	Sequence 30, Appl	216	12.6	36.0	36	1	US-08-198-431-19	Sequence 19, Appl
144	13	37.1	60	4	US-09-451-905-48	Sequence 48, Appl	217	12.6	36.0	36	1	US-08-564-955-19	Sequence 19, Appl
145	13	37.1	71	1	US-08-263-020-9	Sequence 9, Appl	218	12.6	36.0	36	2	US-08-537-874-19	Sequence 19, Appl
146	13	37.1	72	1	US-08-458-423A-80	Sequence 80, Appl	219	12.6	36.0	36	3	US-08-621-859-19	Sequence 19, Appl
147	13	37.1	72	1	US-08-458-424B-80	Sequence 80, Appl	220	12.6	36.0	36	3	US-09-100-886A-19	Sequence 19, Appl
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149	13	37.1	72	5	PCT-US96-08014-80	Sequence 80, Appl	222	12.6	36.0	36	4	US-09-099-015-19	Sequence 19, Appl
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151	13	37.1	73	1	US-08-479-724A-154	Sequence 154, App	224	12.6	36.0	36	4	US-09-233-863-19	Sequence 19, Appl
152	13	37.1	73	3	US-08-472-256B-154	Sequence 154, App	225	12.6	36.0	36	4	US-09-123-508A-19	Sequence 19, Appl
153	13	37.1	73	3	US-08-952-793-154	Sequence 154, App	226	12.6	36.0	36	4	US-09-165-060-19	Sequence 19, Appl
154	13	37.1	73	5	PCT-US96-09455A-154	Sequence 154, App	227	12.6	36.0	36	4	US-09-501-668-19	Sequence 19, Appl
155	13	37.1	81	1	US-08-530-492-113	Sequence 113, App	228	12.6	36.0	36	4	US-09-590-778-19	Sequence 19, Appl
156	13	37.1	81	1	US-08-906-517-113	Sequence 113, App	229	12.6	36.0	36	4	US-09-820-764-24	Sequence 24, Appl
157	13	37.1	87	3	US-08-976-413A-326	Sequence 326, App	230	12.6	36.0	38	1	US-08-259-612A-2	Sequence 2, Appl
158	13	37.1	94	4	US-08-922-793-271	Sequence 271, App	231	12.6	36.0	38	1	US-08-644-291-2	Sequence 2, Appl
159	13	37.1	94	5	PCT-US96-09455A-271	Sequence 271, App	232	12.6	36.0	41	4	US-08-672-213-65	Sequence 65, Appl
160	13	37.1	98	6	5175255-5	Patent No. 5175255	233	12.6	36.0	44	3	US-08-771-623-35	Sequence 25, Appl
161	12.8	36.6	20	4	US-09-167-921-20	Sequence 20, Appl	234	12.6	36.0	45	3	US-08-931-220-31	Sequence 31, Appl
162	12.8	36.6	20	4	US-09-323-743-20	Sequence 20, Appl	235	12.6	36.0	45	3	US-08-931-220-40	Sequence 40, Appl
163	12.8	36.6	22	3	US-09-320-095-13	Sequence 13, Appl	236	12.6	36.0	45	3	US-08-931-220-46	Sequence 46, Appl
164	12.8	36.6	22	4	US-09-523-487-13	Sequence 13, Appl	237	12.6	36.0	45	5	PCT-US95-11723-31	Sequence 31, Appl
165	12.8	36.6	23	3	US-08-973-068-46	Sequence 46, Appl	238	12.6	36.0	45	5	PCT-US95-11723-40	Sequence 40, Appl
166	12.8	36.6	24	3	US-08-722-240-28	Sequence 28, Appl	239	12.6	36.0	45	5	PCT-US95-11723-46	Sequence 46, Appl
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169	12.8	36.6	28	4	US-09-225-928-1171	Sequence 1171, App	242	12.6	36.0	45	5	PCT-US96-05997-46	Sequence 46, Appl
170	12.8	36.6	31	1	US-08-321-080-5	Sequence 5, Appl	243	12.6	36.0	47	1	US-08-384-708A-136	Sequence 136, App
171	12.8	36.6	31	5	PCT-US94-02175-5	Sequence 5, Appl	244	12.6	36.0	47	4	US-08-687-421-136	Sequence 136, App
172	12.8	36.6	39	1	US-08-121-054C-9	Sequence 9, Appl	245	12.6	36.0	61	4	US-08-952-793-362	Sequence 362, App
173	12.8	36.6	39	3	US-08-539-436-9	Sequence 9, Appl	246	12.6	36.0	61	5	PCT-US96-09455A-362	Sequence 362, App

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248	12.6	36.0	71	1	US-08-458-424B-61	Sequence 61, Appl	321	12.4	35.4	83	2	US-08-894-228-10
249	12.6	36.0	71	1	US-08-973-124-61	Sequence 61, Appl	322	12.4	35.4	83	2	US-08-894-228-11
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256	12.6	36.0	100	4	US-08-221-653-25	Sequence 25, Appl	329	12.4	35.4	83	4	US-09-191-521-6
257	12.6	36.0	100	4	US-08-954-395A-24	Sequence 24, Appl	330	12.4	35.4	83	4	US-09-191-521-7
258	12.6	36.0	100	4	US-08-954-395A-26	Sequence 26, Appl	331	12.4	35.4	83	4	US-09-191-521-8
259	12.6	36.0	100	4	US-08-954-395A-28	Sequence 28, Appl	332	12.4	35.4	83	4	US-09-191-521-9
260	12.6	36.0	100	4	US-08-442-144A-25	Sequence 25, Appl	333	12.4	35.4	83	4	US-09-191-521-10
261	12.6	36.0	100	4	US-08-441-970-25	Sequence 25, Appl	334	12.4	35.4	83	4	US-09-191-521-11
262	12.4	35.4	15	4	US-09-081-646-842	Sequence 842, App	335	12.4	35.4	83	4	US-09-191-521-12
263	12.4	35.4	21	2	US-08-869-793-3	Sequence 3, Appl1	336	12.4	35.4	83	4	US-09-191-521-13
264	12.4	35.4	21	3	US-08-981-825-1	Sequence 1, Appl1	337	12.4	35.4	83	4	US-09-191-521-14
265	12.4	35.4	21	4	US-09-480-784-1	Sequence 1, Appl1	338	12.4	35.4	86	1	US-08-471-033-44
266	12.4	35.4	21	4	US-09-045-583-36	Sequence 36, Appl	339	12.4	35.4	86	2	US-08-471-044-44
267	12.4	35.4	23	4	US-09-254-733-30	Sequence 30, Appl	340	12.4	35.4	86	2	US-08-463-483A-44
268	12.4	35.4	24	1	US-08-477-559-10	Sequence 10, Appl	341	12.4	35.4	86	2	US-08-471-046A-44
269	12.4	35.4	24	2	US-08-995-161-10	Sequence 10, Appl	342	12.4	35.4	86	2	US-08-470-568B-44
270	12.4	35.4	24	2	US-09-063-947-10	Sequence 10, Appl	343	12.4	35.4	86	2	US-08-463-334-44
271	12.4	35.4	25	2	US-08-869-793-4	Sequence 4, Appl1	344	12.4	35.4	86	3	US-09-300-529-44
272	12.4	35.4	25	3	US-08-981-825-2	Sequence 2, Appl1	345	12.4	35.4	86	3	US-08-989-251-32
273	12.4	35.4	25	4	US-09-480-784-2	Sequence 2, Appl1	346	12.4	35.4	89	3	US-09-340-250-32
274	12.4	35.4	27	1	US-08-381-280-20	Sequence 20, Appl	347	12.4	35.4	89	3	US-09-528-108-32
275	12.4	35.4	27	2	US-08-445-533-20	Sequence 20, Appl	348	12.4	35.4	90	1	US-08-123-702-12
276	12.4	35.4	27	3	US-09-052-085-20	Sequence 20, Appl	349	12.4	34.9	20	3	US-09-357-071-42
277	12.4	35.4	30	4	US-08-194-560-9	Sequence 9, Appl1	350	12.2	34.9	20	3	US-09-166-186-122
278	12.4	35.4	33	1	US-08-411-795B-156	Sequence 156, App	351	12.2	34.9	20	4	US-09-313-932-122
279	12.4	35.4	33	1	US-08-411-796-156	Sequence 156, App	352	12.2	34.9	24	1	US-09-015-876-17
280	12.4	35.4	33	1	US-08-469-319A-156	Sequence 156, App	353	12.2	34.9	25	4	US-08-943-731-315
281	12.4	35.4	33	5	PCT-US93-11198-156	Sequence 156, App	354	12.2	34.9	26	1	US-08-465-590-124
282	12.4	35.4	33	5	US-08-033-451B-109	Sequence 109, App	355	12.2	34.9	26	2	US-08-747-536-16
283	12.4	35.4	36	2	US-08-487-431-28	Sequence 28, Appl	356	12.2	34.9	26	4	PCT-US93-08743-124
284	12.4	35.4	42	2	US-08-973-629-22	Sequence 22, Appl	357	12.2	34.9	26	5	US-08-998-099-217
285	12.4	35.4	42	3	US-09-091-814-7	Sequence 7, Appl1	358	12.2	34.9	27	3	US-09-253-396A-08
286	12.4	35.4	42	4	US-08-349-696-5	Sequence 5, Appl1	359	12.2	34.9	27	4	PCT-US91-02766-4
287	12.4	35.4	45	1	US-08-233-009-5	Sequence 5, Appl1	360	12.2	34.9	27	5	5219759-8
288	12.4	35.4	45	1	US-08-233-009-29	Sequence 29, Appl	361	12.2	34.9	27	6	US-08-850-613A-7
289	12.4	35.4	45	1	US-08-560-231-5	Sequence 5, Appl1	362	12.2	34.9	30	3	US-09-382-616A-33
290	12.4	35.4	45	1	US-08-080-704A-5	Sequence 5, Appl1	363	12.2	34.9	40	2	US-08-369-829A-10
291	12.4	35.4	45	1	US-08-540-242A-10	Sequence 10, Appl	364	12.2	34.9	30	6	US-08-586-676E-14
292	12.4	35.4	49	5	PCT-US96-01471-10	Sequence 10, Appl	365	12.2	34.9	33	4	US-09-110-517-9
293	12.4	35.4	50	2	US-08-487-431-27	Sequence 27, Appl	366	12.2	34.9	34	4	US-09-400-541-25
294	12.4	35.4	50	3	US-08-973-629-21	Sequence 21, Appl	367	12.2	34.9	36	4	US-09-382-616A-32
295	12.4	35.4	50	4	US-09-091-814-6	Sequence 6, Appl1	368	12.2	34.9	40	2	US-08-369-829A-10
296	12.4	35.4	58	2	US-08-549-211-21	Sequence 21, Appl	369	12.2	34.9	40	2	US-08-586-676E-14
297	12.4	35.4	64	1	US-07-936-163-16	Sequence 16, Appl	370	12.2	34.9	41	1	US-08-110-294A-27
298	12.4	35.4	64	1	US-07-936-163-17	Sequence 17, Appl	371	12.2	34.9	41	1	US-08-389-926-27
299	12.4	35.4	64	4	US-08-728-601A-56	Sequence 56, Appl	372	12.2	34.9	42	1	US-08-223-224-44
300	12.4	35.4	64	4	US-08-729-601A-57	Sequence 57, Appl	373	12.2	34.9	42	1	US-08-722-258-44
301	12.4	35.4	66	2	US-08-406-849-12	Sequence 12, Appl	374	12.2	34.9	42	3	PCT-US95-04468-44
302	12.4	35.4	66	2	US-08-549-211-23	Sequence 23, Appl	375	12.2	34.9	43	4	US-09-387-300-36
303	12.4	35.4	66	2	US-09-056-953-12	Sequence 12, Appl	376	12.2	34.9	47	2	US-08-363-276B-19
304	12.4	35.4	69	2	US-08-560-916-5	Sequence 5, Appl1	377	12.2	34.9	47	2	PCT-US95-16718-19
305	12.4	35.4	69	2	US-08-676-841-5	Sequence 5, Appl1	378	12.2	34.9	47	5	PCT-US92-10421-7
306	12.4	35.4	75	2	US-08-549-211-2	Sequence 2, Appl1	379	12.2	34.9	49	5	US-08-366-490-9
307	12.4	35.4	75	2	US-08-540-211-1	Sequence 1, Appl1	380	12.2	34.9	57	3	US-08-860-483A-10
308	12.4	35.4	76	2	US-09-039-555B-6	Sequence 6, Appl1	381	12.2	34.9	61	4	US-08-483-511-31
309	12.4	35.4	80	3	US-08-989-251-33	Sequence 33, Appl	382	12.2	34.9	61	4	PCT-US93-01009-31
310	12.4	35.4	81	3	US-09-340-250-33	Sequence 33, Appl	383	12.2	34.9	61	5	US-08-261-670-19
311	12.4	35.4	81	3	US-09-528-108-33	Sequence 33, Appl	384	12.2	34.9	62	1	US-09-296-607-1
312	12.4	35.4	81	3	US-08-894-228-3	Sequence 3, Appl1	385	12.2	34.9	62	4	PCT-US93-02115-19
313	12.4	35.4	83	4	US-08-894-228-4	Sequence 4, Appl1	386	12.2	34.9	62	5	US-08-447-169A-97
314	12.4	35.4	83	2	US-08-894-228-5	Sequence 5, Appl1	387	12.2	34.9	65	1	US-08-233-012C-97
315	12.4	35.4	83	2	US-08-894-228-6	Sequence 6, Appl1	388	12.2	34.9	65	2	PCT-US92-06821A-109
316	12.4	35.4	83	2	US-08-894-228-7	Sequence 7, Appl1	389	12.2	34.9	67	5	US-07-744-282C-05
317	12.4	35.4	83	2	US-08-894-228-8	Sequence 8, Appl1	390	12.2	34.9	68	1	US-07-744-282C-06
318	12.4	35.4	83	2	US-08-894-228-9	Sequence 9, Appl1	391	12.2	34.9	68	1	PCT-US92-06821A-108
319	12.4	35.4	83	2	US-08-894-228-10	Sequence 10, Appl	392	12.2	34.9	68	5	

Sequence 9, Appl1	Sequence 10, Appl	Sequence 11, Appl	Sequence 12, Appl	Sequence 13, Appl	Sequence 14, Appl	Sequence 15, Appl	Sequence 16, Appl	Sequence 17, Appl	Sequence 18, Appl	Sequence 19, Appl	Sequence 20, Appl	Sequence 21, Appl	Sequence 22, Appl	Sequence 23, Appl	Sequence 24, Appl	Sequence 25, Appl	Sequence 26, Appl	Sequence 27, Appl	Sequence 28, Appl	Sequence 29, Appl	Sequence 30, Appl	Sequence 31, Appl	Sequence 32, Appl	Sequence 33, Appl	Sequence 34, Appl	Sequence 35, Appl	Sequence 36, Appl	Sequence 37, Appl	Sequence 38, Appl	Sequence 39, Appl	Sequence 40, Appl	Sequence 41, Appl	Sequence 42, Appl	Sequence 43, Appl	Sequence 44, Appl	Sequence 45, Appl	Sequence 46, Appl	Sequence 47, Appl	Sequence 48, Appl	Sequence 49, Appl	Sequence 50, Appl	Sequence 51, Appl	Sequence 52, Appl	Sequence 53, Appl	Sequence 54, Appl	Sequence 55, Appl	Sequence 56, Appl	Sequence 57, Appl	Sequence 58, Appl	Sequence 59, Appl	Sequence 60, Appl	Sequence 61, Appl	Sequence 62, Appl	Sequence 63, Appl	Sequence 64, Appl	Sequence 65, Appl	Sequence 66, Appl	Sequence 67, Appl	Sequence 68, Appl	Sequence 69, Appl	Sequence 70, Appl	Sequence 71, Appl	Sequence 72, Appl	Sequence 73, Appl	Sequence 74, Appl	Sequence 75, Appl	Sequence 76, Appl	Sequence 77, Appl	Sequence 78, Appl	Sequence 79, Appl	Sequence 80, Appl	Sequence 81, Appl	Sequence 82, Appl	Sequence 83, Appl	Sequence 84, Appl	Sequence 85, Appl	Sequence 86, Appl	Sequence 87, Appl	Sequence 88, Appl	Sequence 89, Appl	Sequence 90, Appl	Sequence 91, Appl	Sequence 92, Appl	Sequence 93, Appl	Sequence 94, Appl	Sequence 95, Appl	Sequence 96, Appl	Sequence 97, Appl	Sequence 98, Appl	Sequence 99, Appl	Sequence 100, Appl	Sequence 101, Appl	Sequence 102, Appl	Sequence 103, Appl	Sequence 104, Appl	Sequence 105, Appl	Sequence 106, Appl	Sequence 107, Appl	Sequence 108, Appl	Sequence 109, Appl	Sequence 110, Appl	Sequence 111, Appl	Sequence 112, Appl	Sequence 113, Appl	Sequence 114, Appl	Sequence 115, Appl	Sequence 116, Appl	Sequence 117, Appl	Sequence 118, Appl	Sequence 119, Appl	Sequence 120, Appl	Sequence 121, Appl	Sequence 122, Appl	Sequence 123, Appl	Sequence 124, Appl	Sequence 125, Appl	Sequence 126, Appl	Sequence 127, Appl	Sequence 128, Appl	Sequence 129, Appl	Sequence 130, Appl	Sequence 131, Appl	Sequence 132, Appl	Sequence 133, Appl	Sequence 134, Appl	Sequence 135, Appl	Sequence 136, Appl	Sequence 137, Appl	Sequence 138, Appl	Sequence 139, Appl	Sequence 140, Appl	Sequence 141, Appl	Sequence 142, Appl	Sequence 143, Appl	Sequence 144, Appl	Sequence 145, Appl	Sequence 146, Appl	Sequence 147, Appl	Sequence 148, Appl	Sequence 149, Appl	Sequence 150, Appl	Sequence 151, Appl	Sequence 152, Appl	Sequence 153, Appl	Sequence 154, Appl	Sequence 155, Appl	Sequence 156, Appl	Sequence 157, Appl	Sequence 158, Appl	Sequence 159, Appl	Sequence 160, Appl	Sequence 161, Appl	Sequence 162, Appl	Sequence 163, Appl	Sequence 164, Appl	Sequence 165, Appl	Sequence 166, Appl	Sequence 167, Appl	Sequence 168, Appl	Sequence 169, Appl	Sequence 170, Appl	Sequence 171, Appl	Sequence 172, Appl	Sequence 173, Appl	Sequence 174, Appl	Sequence 175, Appl	Sequence 176, Appl	Sequence 177, Appl	Sequence 178, Appl	Sequence 179, Appl	Sequence 180, Appl	Sequence 181, Appl	Sequence 182, Appl	Sequence 183, Appl	Sequence 184, Appl	Sequence 185, Appl	Sequence 186, Appl	Sequence 187, Appl	Sequence 188, Appl	Sequence 189, Appl	Sequence 190, Appl	Sequence 191, Appl	Sequence 192, Appl	Sequence 193, Appl	Sequence 194, Appl	Sequence 195, Appl	Sequence 196, Appl	Sequence 197, Appl	Sequence 198, Appl	Sequence 199, Appl	Sequence 200, Appl	Sequence 201, Appl	Sequence 202, Appl	Sequence 203, Appl	Sequence 204, Appl	Sequence 205, Appl	Sequence 206, Appl	Sequence 207, Appl	Sequence 208, Appl	Sequence 209, Appl	Sequence 210, Appl	Sequence 211, Appl	Sequence 212, Appl	Sequence 213, Appl	Sequence 214, Appl	Sequence 215, Appl	Sequence 216, Appl	Sequence 217, Appl	Sequence 218, Appl	Sequence 219, Appl	Sequence 220, Appl	Sequence 221, Appl	Sequence 222, Appl	Sequence 223, Appl	Sequence 224, Appl
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C 393	12.2	34.9	69	4	US-09-363-939A-25	Sequence 25, App1	466	12	34.3	34	3	US-08-834-314-19	Sequence 19, App1
C 394	12.2	34.9	70	3	US-09-205-428-17	Sequence 17, App1	467	12	34.3	35	1	US-08-375-235-6	Sequence 6, App1
C 395	12.2	34.9	70	3	US-09-205-428-20	Sequence 20, App1	468	12	34.3	36	2	US-08-805-918-23	Sequence 23, App1
C 396	12.2	34.9	70	4	US-09-625-188-31	Sequence 31, App1	469	12	34.3	36	2	US-08-897-340-24	Sequence 24, App1
C 397	12.2	34.9	71	1	US-07-982-712-19	Sequence 19, App1	470	12	34.3	36	3	US-09-352-329-24	Sequence 24, App1
C 398	12.2	34.9	71	4	US-08-952-793-332	Sequence 332, App1	C 471	12	34.3	36	4	US-09-333-348B-7	Sequence 7, App1
C 399	12.2	34.9	71	5	PCT-US96-09455A-332	Sequence 332, App	C 472	12	34.3	37	1	US-08-197-770-22	Sequence 22, App1
C 400	12.2	34.9	73	1	US-08-434-001-37	Sequence 37, App1	C 473	12	34.3	37	1	US-08-049-264C-36	Sequence 36, App1
C 401	12.2	34.9	73	1	US-08-434-585-37	Sequence 37, App1	C 474	12	34.3	37	1	US-08-476-562-36	Sequence 36, App1
C 402	12.2	34.9	73	1	US-08-434-425-37	Sequence 37, App1	C 475	12	34.3	37	1	US-08-476-562-36	Sequence 36, App1
C 403	12.2	34.9	73	2	US-08-437-667-37	Sequence 37, App1	C 476	12	34.3	37	1	US-08-476-562-36	Sequence 36, App1
C 404	12.2	34.9	73	3	US-08-965-955-37	Sequence 37, App1	C 477	12	34.3	37	1	US-08-479-723A-36	Sequence 36, App1
C 405	12.2	34.9	73	3	US-08-945-909-37	Sequence 37, App1	C 478	12	34.3	37	1	US-08-479-723A-39	Sequence 39, App1
C 406	12.2	34.9	73	5	PCT-US96-06060-37	Sequence 37, App1	C 479	12	34.3	37	5	PCT-US94-04310-36	Sequence 36, App1
C 407	12.2	34.9	74	1	US-07-920-519-25	Sequence 25, App1	C 480	12	34.3	37	5	PCT-US94-04310-39	Sequence 39, App1
C 408	12.2	34.9	74	1	US-08-314-586-25	Sequence 25, App1	C 481	12	34.3	38	3	US-08-445-463C-123	Sequence 123, App
C 409	12.2	34.9	74	3	US-08-115-753-27	Sequence 27, App1	C 482	12	34.3	38	3	US-08-445-463C-123	Sequence 123, App
C 410	12.2	34.9	75	2	US-07-916-098A-20	Sequence 20, App1	C 483	12	34.3	38	5	PCT-US94-03437-123	Sequence 123, App
C 411	12.2	34.9	77	1	US-07-910-528-7	Sequence 7, App1	C 484	12	34.3	39	1	US-08-106-507-4	Sequence 4, App1
C 412	12.2	34.9	77	1	US-08-348-972-7	Sequence 7, App1	C 485	12	34.3	39	1	US-08-726-528B-6	Sequence 6, App1
C 413	12.2	34.9	77	1	US-08-477-530-11	Sequence 11, App1	C 486	12	34.3	40	1	US-08-530-492-73	Sequence 73, App1
C 414	12.2	34.9	77	1	US-08-477-830-11	Sequence 11, App1	C 487	12	34.3	40	1	US-08-137-117D-17	Sequence 17, App1
C 415	12.2	34.9	77	1	US-07-907-710A-14	Sequence 14, App1	C 488	12	34.3	40	1	US-08-436-717-17	Sequence 17, App1
C 416	12.2	34.9	81	1	US-08-238-863-80	Sequence 80, App1	C 489	12	34.3	40	2	US-08-553-501A-17	Sequence 17, App1
C 417	12.2	34.9	81	1	US-08-238-863-80	Sequence 80, App1	C 490	12	34.3	40	2	US-08-765-783A-17	Sequence 17, App1
C 418	12.2	34.9	81	1	US-08-238-863-81	Sequence 81, App1	C 491	12	34.3	40	3	US-08-921-100-17	Sequence 17, App1
C 419	12.2	34.9	81	1	US-08-209-182C-14	Sequence 14, App1	C 492	12	34.3	40	3	US-08-880-142-17	Sequence 17, App1
C 420	12.2	34.9	81	1	US-08-443-407-80	Sequence 80, App1	C 493	12	34.3	40	3	US-08-902-201-17	Sequence 17, App1
C 421	12.2	34.9	81	1	US-08-443-407-81	Sequence 81, App1	C 494	12	34.3	40	3	US-09-205-231-17	Sequence 17, App1
C 422	12.2	34.9	81	5	PCT-US95-05600-224	Sequence 224, App	C 495	12	34.3	40	4	US-08-606-517-73	Sequence 73, App1
C 423	12.2	34.9	81	5	PCT-US95-05600-225	Sequence 225, App	C 496	12	34.3	40	4	US-08-646-265A-17	Sequence 17, App1
C 424	12.2	34.9	82	5	US-08-921-887-34	Sequence 34, App1	C 497	12	34.3	40	4	US-09-416-557-17	Sequence 17, App1
C 425	12.2	34.9	83	1	US-08-398-617-9	Sequence 9, App1	C 498	12	34.3	42	3	US-08-109-037-6	Sequence 6, App1
C 426	12.2	34.9	83	2	US-08-398-617-9	Sequence 9, App1	C 499	12	34.3	42	3	US-08-109-037-73	Sequence 73, App1
C 427	12.2	34.9	83	4	US-08-397-303-9	Sequence 9, App1	C 500	12	34.3	42	3	US-08-109-037-75	Sequence 75, App1
C 428	12.2	34.9	88	1	US-08-398-617-1	Sequence 1, App1	C 501	12	34.3	42	3	US-09-331-581-10	Sequence 10, App1
C 429	12.2	34.9	88	2	US-08-397-303-1	Sequence 1, App1	C 502	12	34.3	42	3	US-09-331-581-10	Sequence 10, App1
C 430	12.2	34.9	88	4	US-08-397-303-1	Sequence 1, App1	C 503	12	34.3	42	3	US-09-331-581-16	Sequence 16, App1
C 431	12.2	34.9	91	4	US-08-050-482A-19	Sequence 19, App1	C 504	12	34.3	42	6	5231166-15	Patent No. 5231166
C 432	12.2	34.9	91	4	US-08-050-482A-20	Sequence 20, App1	C 505	12	34.3	43	1	US-08-540-242A-9	Sequence 9, App1
C 433	12.2	34.9	96	1	US-08-361-708A-25	Sequence 25, App1	C 506	12	34.3	43	5	PCT-US96-01471-9	Sequence 9, App1
C 434	12.2	34.9	96	1	US-08-153-071-3	Sequence 3, App1	C 507	12	34.3	46	1	US-08-232-537-4	Sequence 4, App1
C 435	12.2	34.9	96	1	US-08-536-277-25	Sequence 25, App1	C 508	12	34.3	46	1	US-08-983-035A-52	Sequence 52, App1
C 436	12.2	34.9	96	1	US-08-609-271-10	Sequence 10, App1	C 509	12	34.3	48	5	PCT-US94-07779-5	Sequence 5, App1
C 437	12.2	34.9	96	2	US-08-438-511-3	Sequence 3, App1	C 510	12	34.3	51	2	US-08-980-071-16	Sequence 16, App1
C 438	12.2	34.9	96	2	US-08-487-431-6	Sequence 6, App1	C 511	12	34.3	51	2	US-08-980-071-24	Sequence 24, App1
C 439	12.2	34.9	96	3	US-08-188-374-10	Sequence 10, App1	C 512	12	34.3	51	2	US-08-757-536-16	Sequence 16, App1
C 440	12.2	34.9	96	3	US-08-973-629-6	Sequence 6, App1	C 513	12	34.3	51	2	US-08-757-536-24	Sequence 24, App1
C 441	12.2	34.9	97	3	US-09-106-638-6	Sequence 6, App1	C 514	12	34.3	51	3	US-09-314-093-16	Sequence 16, App1
C 442	12.2	34.9	99	4	US-08-737-608-7	Sequence 7, App1	C 515	12	34.3	51	3	US-09-314-093-24	Sequence 24, App1
C 443	12.2	34.9	100	4	US-08-954-395A-26	Sequence 26, App1	C 516	12	34.3	51	3	US-09-337-633-24	Sequence 24, App1
C 444	12.2	34.3	18	3	US-08-577-081A-18	Sequence 18, App1	C 517	12	34.3	51	3	US-08-482-882-60	Sequence 60, App1
C 445	12.2	34.3	19	3	US-08-652-265-37	Sequence 37, App1	C 518	12	34.3	51	4	US-09-251-885-16	Sequence 16, App1
C 446	12.2	34.3	19	4	US-08-834-497A-37	Sequence 37, App1	C 519	12	34.3	51	4	US-09-251-885-24	Sequence 24, App1
C 447	12.2	34.3	19	4	US-09-503-444A-37	Sequence 37, App1	C 520	12	34.3	51	4	US-09-337-633-16	Sequence 16, App1
C 448	12.2	34.3	20	3	US-08-765-332-204	Sequence 204, App	C 521	12	34.3	51	4	US-09-337-633-24	Sequence 24, App1
C 449	12.2	34.3	20	4	US-08-943-731-590	Sequence 590, App	C 522	12	34.3	52	1	US-08-482-882-60	Sequence 60, App1
C 450	12.2	34.3	20	4	US-09-448-894-204	Sequence 204, App	C 523	12	34.3	52	1	US-08-475-680-60	Sequence 60, App1
C 451	12.2	34.3	23	2	US-08-894-228-16	Sequence 16, App1	C 524	12	34.3	52	2	US-08-943-136-19	Sequence 19, App1
C 452	12.2	34.3	23	4	US-09-191-521-16	Sequence 16, App1	C 525	12	34.3	52	2	US-08-487-113D-60	Sequence 60, App1
C 453	12.2	34.3	24	3	US-09-040-005-5	Sequence 5, App1	C 526	12	34.3	52	2	US-08-473-503-60	Sequence 60, App1
C 454	12.2	34.3	24	4	US-09-262-773-205	Sequence 205, App	C 527	12	34.3	52	2	US-08-483-932-60	Sequence 60, App1
C 455	12.2	34.3	28	1	US-08-915-003-4	Sequence 4, App1	C 528	12	34.3	52	2	US-08-720-420A-60	Sequence 60, App1
C 456	12.2	34.3	28	2	US-08-642-247-4	Sequence 4, App1	C 529	12	34.3	52	3	US-08-714-017-60	Sequence 60, App1
C 457	12.2	34.3	28	2	US-08-859-998-942	Sequence 942, App	C 530	12	34.3	52	4	US-08-475-680-60	Sequence 60, App1
C 458	12.2	34.3	28	4	US-08-672-213-53	Sequence 53, App1	C 531	12	34.3	52	4	US-08-943-136-19	Sequence 19, App1
C 459	12.2	34.3	28	4	US-08-973-131-42	Sequence 42, App1	C 532	12	34.3	52	4	US-08-973-518-19	Sequence 19, App1
C 460	12.2	34.3	28	4	US-09-225-928-942	Sequence 942, App	C 533	12	34.3	53	2	US-08-860-174A-17	Sequence 17, App1
C 461	12.2	34.3	30	1	US-08-468-036-47	Sequence 47, App1	C 534	12	34.3	53	4	US-09-171-025-10	Sequence 10, App1
C 462	12.2	34.3	30	2	US-08-376-843-47	Sequence 47, App1	C 535	12	34.3	57	1	US-07-640-473-3	Sequence 3, App1
C 463	12.2	34.3	31	3	US-09-032-894-107	Sequence 107, App	C 536	12	34.3	57	1	US-07-908-317-22	Sequence 22, App1
C 464	12.2	34.3	31	4	US-09-031-626-107	Sequence 107, App	C 537	12	34.3	59	1	PCT-US93-06111-22	Sequence 22, App1
C 465	12.2	34.3	34	3	US-08-646-789A-75	Sequence 75, App1	C 538	12	34.3	59	4	US-08-530-492-88	Sequence 88, App1

539	12	34.3	60	1	US-08-219-012-76	Sequence 76, Appl	C 612	11.8	33.7	38	3	US-08-890-719-15	Sequence 15, Appl
540	12	34.3	60	4	US-08-687-421-264	Sequence 26, App	613	11.8	33.7	38	4	US-09-078-199-27	Sequence 27, Appl
541	12	34.3	70	1	US-08-434-001-86	Sequence 86, Appl	614	11.8	33.7	38	4	US-09-078-199-27	Sequence 27, Appl
542	12	34.3	70	1	US-08-433-585-86	Sequence 86, Appl	615	11.8	33.7	38	4	US-09-366-971-27	Sequence 27, Appl
543	12	34.3	70	2	US-08-434-425-86	Sequence 86, Appl	616	11.8	33.7	38	4	US-09-366-971-27	Sequence 27, Appl
544	12	34.3	70	2	US-08-437-667-86	Sequence 86, Appl	617	11.8	33.7	40	4	US-07-661-370-6	Sequence 6, Appl1
545	12	34.3	70	3	US-08-906-955-86	Sequence 86, Appl	618	11.8	33.7	41	1	US-08-375-116A-3	Sequence 3, Appl1
546	12	34.3	70	3	US-08-945-909-86	Sequence 86, Appl	619	11.8	33.7	41	3	US-08-813-507-34	Sequence 34, Appl1
547	12	34.3	70	5	PCT-US96-06060-86	Sequence 86, Appl	620	11.8	33.7	41	4	US-09-239-303-5	Sequence 5, Appl1
548	12	34.3	71	4	US-08-952-793-309	Sequence 309, App	621	11.8	33.7	42	1	US-09-464-433-34	Sequence 34, Appl
549	12	34.3	71	4	US-08-952-793-311	Sequence 311, App	622	11.8	33.7	42	1	US-07-834-539A-40	Sequence 40, Appl
550	12	34.3	71	5	PCT-US96-09455A-309	Sequence 309, App	623	11.8	33.7	42	1	US-08-053-131-48	Sequence 48, Appl
551	12	34.3	71	5	PCT-US96-09455A-311	Sequence 311, App	624	11.8	33.7	42	1	US-08-643-641-48	Sequence 48, Appl
552	12	34.3	75	2	US-08-469-537A-63	Sequence 63, Appl	625	11.8	33.7	42	1	US-07-853-408B-48	Sequence 48, Appl
553	12	34.3	76	4	US-08-602-999A-162	Sequence 162, App	626	11.8	33.7	42	1	US-08-096-762-48	Sequence 48, Appl
554	12	34.3	76	4	US-08-602-999A-454	Sequence 454, App	627	11.8	33.7	42	2	US-08-800-353-40	Sequence 40, Appl
555	12	34.3	77	1	US-08-477-530-5	Sequence 5, Appl1	628	11.8	33.7	42	2	US-08-308-885-48	Sequence 48, Appl
556	12	34.3	77	1	US-08-477-530-5	Sequence 5, Appl1	629	11.8	33.7	42	2	US-08-308-885-48	Sequence 48, Appl
557	12	34.3	77	1	US-08-477-530-5	Sequence 5, Appl1	630	11.8	33.7	42	4	US-09-042-353-211	Sequence 211, App
558	12	34.3	79	1	US-08-384-708A-209	Sequence 209, App	631	11.8	33.7	42	5	US-08-758-417A-59	Sequence 59, Appl
559	12	34.3	79	2	US-08-470-939-7	Sequence 7, Appl1	632	11.8	33.7	42	5	PCT-US92-06185-40	Sequence 40, Appl
560	12	34.3	79	4	US-08-687-421-301	Sequence 301, App	633	11.8	33.7	44	1	US-08-096-762-209	Sequence 209, App
561	12	34.3	79	5	PCT-US96-09452-7	Sequence 7, Appl1	634	11.8	33.7	44	3	US-09-218-849-21	Sequence 21, Appl
562	12	34.3	80	3	US-08-718-904-110	Sequence 110, App	635	11.8	33.7	44	3	US-09-218-849-22	Sequence 22, Appl
563	12	34.3	87	1	US-08-433-126A-171	Sequence 171, App	636	11.8	33.7	44	4	US-09-042-353-323	Sequence 323, App
564	12	34.3	87	1	US-08-433-126A-171	Sequence 171, App	637	11.8	33.7	44	4	US-08-758-417A-171	Sequence 171, App
565	12	34.3	87	3	US-08-976-413A-171	Sequence 171, App	638	11.8	33.7	45	1	US-08-083-948-4	Sequence 4, Appl1
566	12	34.3	87	5	PCT-US96-06059-171	Sequence 171, App	639	11.8	33.7	45	1	US-08-393-785-4	Sequence 4, Appl1
567	12	34.3	91	4	US-08-905-223-161	Sequence 161, App	640	11.8	33.7	45	1	US-08-475-684-4	Sequence 4, Appl1
568	12	34.3	91	4	US-09-025-769B-303	Sequence 303, App	641	11.8	33.7	45	1	US-08-171-389-66	Sequence 66, Appl
569	12	34.3	96	3	US-08-484-322-48	Sequence 48, Appl1	642	11.8	33.7	45	1	US-08-256-368-5	Sequence 5, Appl1
570	12	34.3	97	3	US-08-136-277-8	Sequence 8, Appl1	643	11.8	33.7	45	1	US-08-256-368-6	Sequence 6, Appl1
571	12	34.3	97	2	US-08-479-403-8	Sequence 8, Appl1	644	11.8	33.7	45	1	US-08-123-966-66	Sequence 66, Appl
572	12	34.3	97	3	US-08-835-734-8	Sequence 8, Appl1	645	11.8	33.7	45	1	US-08-712-057-4	Sequence 4, Appl1
573	11.8	33.7	17	2	US-08-485-689-45	Sequence 45, Appl	646	11.8	33.7	45	2	US-08-475-228A-66	Sequence 66, Appl
574	11.8	33.7	17	2	US-08-476-021A-45	Sequence 45, Appl	647	11.8	33.7	45	2	US-08-716-308-9	Sequence 9, Appl1
575	11.8	33.7	17	2	US-08-476-608B-45	Sequence 45, Appl	648	11.8	33.7	45	2	US-08-716-308-10	Sequence 10, Appl
576	11.8	33.7	17	4	US-08-476-423A-45	Sequence 45, Appl	649	11.8	33.7	45	3	US-08-482-080A-66	Sequence 66, Appl
577	11.8	33.7	17	4	US-08-584-040-3945	Sequence 3945, App	650	11.8	33.7	45	4	US-09-423-439-49	Sequence 49, Appl
578	11.8	33.7	18	1	US-08-531-556-122	Sequence 122, App	651	11.8	33.7	45	5	PCT-US93-12388-66	Sequence 66, Appl
579	11.8	33.7	18	2	US-08-337-766A-73	Sequence 73, Appl	652	11.8	33.7	47	2	US-08-659-567-16	Sequence 16, Appl
580	11.8	33.7	18	2	US-08-690-734A-81	Sequence 81, Appl	653	11.8	33.7	48	3	US-08-731-512-4	Sequence 4, Appl1
581	11.8	33.7	18	3	US-08-289-376-45	Sequence 45, Appl	654	11.8	33.7	48	4	US-08-915-132-42	Sequence 42, Appl
582	11.8	33.7	18	3	US-08-742-185-81	Sequence 81, Appl	655	11.8	33.7	48	4	US-09-461-657-458	Sequence 458, App
583	11.8	33.7	19	2	US-08-485-689-44	Sequence 44, Appl	656	11.8	33.7	48	5	PCT-US96-07627-40	Sequence 40, Appl1
584	11.8	33.7	19	2	US-08-476-021A-44	Sequence 44, Appl	657	11.8	33.7	49	1	US-07-643-313-9	Sequence 9, Appl1
585	11.8	33.7	19	2	US-08-478-608B-44	Sequence 44, Appl	658	11.8	33.7	50	1	US-08-171-389-531	Sequence 531, App
586	11.8	33.7	19	4	US-08-738-652-50	Sequence 50, Appl	659	11.8	33.7	50	1	US-08-207-901-26	Sequence 26, Appl
587	11.8	33.7	19	4	US-09-030-701-22	Sequence 22, Appl	660	11.8	33.7	50	1	US-08-123-926-531	Sequence 531, App
588	11.8	33.7	19	4	US-08-476-423A-44	Sequence 44, Appl	661	11.8	33.7	50	2	US-08-475-228A-531	Sequence 531, App
589	11.8	33.7	19	4	US-08-960-774-41	Sequence 41, Appl	662	11.8	33.7	50	2	US-08-541-033A-9	Sequence 9, Appl1
590	11.8	33.7	20	1	US-08-328-314-15	Sequence 15, Appl	663	11.8	33.7	50	2	US-08-828-451-9	Sequence 9, Appl1
591	11.8	33.7	20	1	US-08-731-045-15	Sequence 15, Appl	664	11.8	33.7	50	3	US-08-482-080A-531	Sequence 531, App
592	11.8	33.7	20	1	US-08-782-047-21	Sequence 21, Appl	665	11.8	33.7	50	3	US-08-836-922-12	Sequence 12, Appl
593	11.8	33.7	20	2	US-08-117-952-468	Sequence 468, App	666	11.8	33.7	50	5	PCT-US93-12388-531	Sequence 531, App
594	11.8	33.7	20	3	US-08-924-870A-21	Sequence 21, Appl	667	11.8	33.7	51	1	US-07-630-288A-22	Sequence 22, Appl
595	11.8	33.7	21	2	US-08-541-033A-12	Sequence 12, Appl	668	11.8	33.7	51	1	US-08-466-049-22	Sequence 22, Appl
596	11.8	33.7	21	2	US-08-828-451-12	Sequence 12, Appl	669	11.8	33.7	51	4	US-08-915-152-28	Sequence 28, Appl
597	11.8	33.7	21	4	US-09-485-636-22	Sequence 22, Appl	670	11.8	33.7	51	5	PCT-US96-07627-40	Sequence 30, Appl
598	11.8	33.7	22	4	US-09-461-687-67	Sequence 67, Appl	671	11.8	33.7	54	3	US-08-836-922-11	Sequence 11, Appl
599	11.8	33.7	25	4	US-09-101-629A-20	Sequence 20, Appl	672	11.8	33.7	54	4	US-09-423-439-28	Sequence 28, Appl
600	11.8	33.7	26	2	US-08-853-217-17	Sequence 17, Appl	673	11.8	33.7	55	1	US-07-630-288A-23	Sequence 23, Appl
601	11.8	33.7	26	2	US-08-853-217-18	Sequence 18, Appl	674	11.8	33.7	55	1	US-08-466-049-23	Sequence 23, Appl
602	11.8	33.7	26	4	US-09-302-334-4	Sequence 4, Appl1	675	11.8	33.7	57	1	US-07-630-288A-24	Sequence 24, Appl
603	11.8	33.7	27	2	US-08-659-567-5	Sequence 5, Appl1	676	11.8	33.7	57	1	US-08-466-049-24	Sequence 24, Appl
604	11.8	33.7	27	4	US-08-891-282A-82	Sequence 82, Appl	677	11.8	33.7	58	3	US-09-173-941-118	Sequence 118, App
605	11.8	33.7	33	3	US-08-181-492B-15	Sequence 15, Appl	678	11.8	33.7	58	4	US-08-123-722A-5	Sequence 5, Appl1
606	11.8	33.7	33	5	PCT-US95-00408-15	Sequence 15, Appl	679	11.8	33.7	59	1	US-08-209-747-51	Sequence 51, Appl1
607	11.8	33.7	34	1	US-08-434-503-48	Sequence 48, Appl	680	11.8	33.7	59	4	US-08-458-298-51	Sequence 51, Appl1
608	11.8	33.7	34	1	US-08-207-169A-13	Sequence 13, Appl	681	11.8	33.7	59	4	US-09-202-976-5	Sequence 5, Appl1
609	11.8	33.7	36	2	US-07-724-500B-6	Sequence 6, Appl1	682	11.8	33.7	60	1	US-08-346-666-3	Sequence 3, Appl1
610	11.8	33.7	36	2	US-08-461-418B-14	Sequence 14, Appl	683	11.8	33.7	60	1	US-08-233-009-3	Sequence 3, Appl1
611	11.8	33.7	37	1	US-08-197-770-23	Sequence 23, Appl	684	11.8	33.7	60	1	US-08-560-221-3	Sequence 3, Appl1

c 685	11.8	33.7	60	2	US-08-053-451B-160	Sequence 160, App	c 758	11.8	33.7	96	4	US-09-042-353-255	Sequence 259, App
c 686	11.8	33.7	60	2	US-08-053-451B-170	Sequence 170, App	c 759	11.8	33.7	96	4	US-08-758-417A-107	Sequence 107, App
c 687	11.8	33.7	60	4	US-09-080-704A-3	Sequence 3, Appl	c 760	11.8	33.7	96	5	PCR-US92-10963-142	Sequence 142, App
c 688	11.8	33.7	60	5	PCR-US95-11985A-7	Sequence 7, Appl	c 761	11.8	33.7	99	1	US-08-053-131-139	Sequence 139, App
c 689	11.8	33.7	61	3	US-08-784-582-78	Sequence 78, Appl	c 762	11.8	33.7	99	1	US-08-645-641-139	Sequence 139, App
c 690	11.8	33.7	61	3	US-08-784-582-79	Sequence 79, Appl	c 763	11.8	33.7	99	1	US-07-853-408B-139	Sequence 139, App
c 691	11.8	33.7	61	4	US-08-785-271-55	Sequence 55, Appl	c 764	11.8	33.7	99	1	US-08-096-762-139	Sequence 139, App
c 692	11.8	33.7	61	4	US-08-785-271-56	Sequence 56, Appl	c 765	11.8	33.7	99	2	US-08-308-865-139	Sequence 139, App
c 693	11.8	33.7	61	4	US-09-364-539-56	Sequence 56, Appl	c 766	11.8	33.7	99	4	US-09-042-353-256	Sequence 256, App
c 694	11.8	33.7	66	1	US-07-916-034-21	Sequence 21, Appl	c 767	11.8	33.7	99	4	US-08-758-417A-104	Sequence 104, App
c 695	11.8	33.7	70	1	US-08-317-403A-31	Sequence 31, Appl	c 768	11.8	33.7	99	5	PCR-US92-10963-139	Sequence 139, App
c 696	11.8	33.7	70	1	US-08-471-985A-31	Sequence 31, Appl	c 769	11.8	33.7	100	4	US-09-465-355-20	Sequence 20, Appl
c 697	11.8	33.7	70	1	US-08-374-641-1	Sequence 1, Appl	c 770	11.6	33.1	18	1	US-08-468-580-37	Sequence 37, Appl
c 698	11.8	33.7	70	2	US-08-465-591A-37	Sequence 37, Appl	c 771	11.6	33.1	18	4	US-08-643-212-59	Sequence 59, Appl
c 699	11.8	33.7	70	2	US-08-465-594A-37	Sequence 37, Appl	c 772	11.6	33.1	18	5	PCR-US95-03731-37	Sequence 37, Appl
c 700	11.8	33.7	70	2	US-08-477-527A-28	Sequence 28, Appl	c 773	11.6	33.1	19	1	US-08-605-089-11	Sequence 11, Appl
c 701	11.8	33.7	70	2	US-08-477-527A-41	Sequence 41, Appl	c 774	11.6	33.1	20	4	US-09-513-728B-63	Sequence 63, Appl
c 702	11.8	33.7	70	3	US-08-481-710-28	Sequence 28, Appl	c 775	11.6	33.1	20	4	US-09-487-368A-208	Sequence 208, App
c 703	11.8	33.7	70	3	US-08-481-710-41	Sequence 41, Appl	c 776	11.6	33.1	21	1	US-07-972-791-12	Sequence 12, Appl
c 704	11.8	33.7	70	3	US-08-973-124-222	Sequence 222, App	c 777	11.6	33.1	21	1	US-08-473-157A-6	Sequence 6, Appl
c 705	11.8	33.7	70	5	PCR-US95-12401A-31	Sequence 31, Appl	c 778	11.6	33.1	21	4	US-09-085-476-4	Sequence 4, Appl
c 706	11.8	33.7	70	5	PCR-US96-08014-222	Sequence 222, App	c 779	11.6	33.1	21	6	5310649-5	Patent No. 5310649
c 707	11.8	33.7	70	5	PCR-US96-09537-28	Sequence 28, Appl	c 780	11.6	33.1	22	2	US-08-117-955-78	Sequence 78, Appl
c 708	11.8	33.7	70	5	PCR-US96-09537-41	Sequence 41, Appl	c 781	11.6	33.1	22	1	US-08-674-168-22	Sequence 22, Appl
c 709	11.8	33.7	71	4	US-08-952-793-361	Sequence 361, Appl	c 782	11.6	33.1	23	3	US-08-985-908-8	Sequence 8, Appl
c 710	11.8	33.7	71	5	PCR-US96-09455A-361	Sequence 361, Appl	c 783	11.6	33.1	23	3	US-08-852-730-21	Sequence 21, Appl
c 711	11.8	33.7	72	1	US-08-328-152A-19	Sequence 19, Appl	c 784	11.6	33.1	23	4	US-08-985-916-19	Sequence 19, Appl
c 712	11.8	33.7	72	5	PCR-US91-02766-9	Sequence 9, Appl	c 785	11.6	33.1	24	1	US-08-337-268A-9	Sequence 9, Appl
c 713	11.8	33.7	72	5	PCR-US91-02766-11	Sequence 11, Appl	c 786	11.6	33.1	24	1	US-08-337-268A-14	Sequence 14, Appl
c 714	11.8	33.7	72	6	5219759-12	Patent No. 5219759	c 787	11.6	33.1	24	1	US-08-484-570A-9	Sequence 9, Appl
c 715	11.8	33.7	72	6	5219759-13	Patent No. 5219759	c 788	11.6	33.1	24	1	US-08-484-570A-14	Sequence 14, Appl
c 716	11.8	33.7	73	2	US-08-179-557-8	Sequence 8, Appl	c 789	11.6	33.1	24	3	US-09-000-630C-14	Sequence 14, Appl
c 717	11.8	33.7	73	2	US-07-989-847-24	Sequence 24, Appl	c 790	11.6	33.1	24	3	US-08-379-452-11	Sequence 11, Appl
c 718	11.8	33.7	73	3	US-08-981-601-11	Sequence 11, Appl	c 791	11.6	33.1	24	3	US-08-862-730C-14	Sequence 14, Appl
c 719	11.8	33.7	73	4	US-08-469-411-24	Sequence 24, Appl	c 792	11.6	33.1	24	3	US-09-409-670-11	Sequence 11, Appl
c 720	11.8	33.7	74	3	US-09-173-941-116	Sequence 116, Appl	c 793	11.6	33.1	25	3	US-08-155-938-15	Sequence 15, Appl
c 721	11.8	33.7	75	1	US-08-219-012-87	Sequence 87, Appl	c 794	11.6	33.1	25	3	US-08-155-938-16	Sequence 16, Appl
c 722	11.8	33.7	75	1	US-08-687-421-275	Sequence 275, Appl	c 795	11.6	33.1	25	3	US-08-155-938-19	Sequence 19, Appl
c 723	11.8	33.7	77	4	US-07-916-034-23	Sequence 23, Appl	c 796	11.6	33.1	25	3	US-08-155-938-20	Sequence 20, Appl
c 724	11.8	33.7	77	4	US-09-364-539-121	Sequence 121, Appl	c 797	11.6	33.1	27	1	US-08-274-661B-7	Sequence 7, Appl
c 725	11.8	33.7	79	1	US-08-384-708A-213	Sequence 213, App	c 798	11.6	33.1	27	5	PCR-US93-03967-7	Sequence 39, Appl
c 726	11.8	33.7	79	1	US-08-384-708A-220	Sequence 220, App	c 799	11.6	33.1	28	1	US-08-467-420A-39	Sequence 39, Appl
c 727	11.8	33.7	79	2	US-08-470-939-17	Sequence 17, Appl	c 800	11.6	33.1	28	1	US-08-470-939-18	Sequence 39, Appl
c 728	11.8	33.7	79	4	US-08-687-421-305	Sequence 305, App	c 801	11.6	33.1	28	1	US-08-667-769A-39	Sequence 39, Appl
c 729	11.8	33.7	79	4	US-08-687-421-312	Sequence 312, App	c 802	11.6	33.1	28	2	US-08-667-769A-39	Sequence 39, Appl
c 730	11.8	33.7	79	5	PCR-US96-09452-17	Sequence 17, Appl	c 803	11.6	33.1	28	2	US-08-940-371-39	Sequence 39, Appl
c 731	11.8	33.7	81	2	US-07-989-847-23	Sequence 23, Appl	c 804	11.6	33.1	28	5	PCR-US95-0617-39	Sequence 39, Appl
c 732	11.8	33.7	81	4	US-08-469-411-23	Sequence 23, Appl	c 805	11.6	33.1	29	1	US-08-353-751-11	Sequence 11, Appl
c 733	11.8	33.7	84	1	US-08-209-747-50	Sequence 50, Appl	c 806	11.6	33.1	29	2	US-08-607-631-4	Sequence 4, Appl
c 734	11.8	33.7	84	1	US-08-458-298-50	Sequence 50, Appl	c 807	11.6	33.1	30	1	US-08-102-567-26	Sequence 26, Appl
c 735	11.8	33.7	86	1	US-08-053-131-123	Sequence 123, App	c 808	11.6	33.1	30	1	US-08-198-670A-15	Sequence 15, Appl
c 736	11.8	33.7	86	1	US-08-645-641-123	Sequence 123, App	c 809	11.6	33.1	30	2	US-08-117-952-560	Sequence 560, App
c 737	11.8	33.7	86	1	US-07-853-408B-123	Sequence 123, App	c 810	11.6	33.1	30	3	US-08-462-947-26	Sequence 26, Appl
c 738	11.8	33.7	86	1	US-08-096-762-123	Sequence 123, App	c 811	11.6	33.1	30	4	PCR-US93-09605-15	Sequence 15, Appl
c 739	11.8	33.7	86	2	US-08-308-865-123	Sequence 123, App	c 812	11.6	33.1	30	5	US-09-349-627-5	Sequence 5, Appl
c 740	11.8	33.7	86	4	US-09-564-805-17	Sequence 17, Appl	c 813	11.6	33.1	31	1	US-08-390-850-101	Sequence 101, App
c 741	11.8	33.7	86	5	PCR-US92-10963-123	Sequence 123, App	c 814	11.6	33.1	31	1	US-08-467-420A-40	Sequence 40, Appl
c 742	11.8	33.7	87	3	US-09-184-658-58	Sequence 58, Appl	c 815	11.6	33.1	31	1	US-08-470-110A-40	Sequence 40, Appl
c 743	11.8	33.7	87	4	US-09-042-353-240	Sequence 240, App	c 816	11.6	33.1	31	1	US-08-353-751-10	Sequence 10, Appl
c 744	11.8	33.7	87	4	US-08-758-417A-88	Sequence 88, Appl	c 817	11.6	33.1	31	1	US-08-435-634-101	Sequence 101, App
c 745	11.8	33.7	91	2	US-08-679-522D-9	Sequence 9, Appl	c 818	11.6	33.1	31	1	US-08-667-769A-40	Sequence 40, Appl
c 746	11.8	33.7	91	2	US-08-664-863B-13	Sequence 13, Appl	c 819	11.6	33.1	31	2	US-08-940-371-40	Sequence 40, Appl
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c 748	11.8	33.7	91	3	US-08-784-582-77	Sequence 77, Appl	c 821	11.6	33.1	31	3	US-08-637-647-40	Sequence 40, Appl
c 749	11.8	33.7	91	3	US-09-141-401-9	Sequence 9, Appl	c 822	11.6	33.1	31	5	PCR-US95-17082A-40	Sequence 40, Appl
c 750	11.8	33.7	91	4	US-08-785-271-53	Sequence 53, Appl	c 823	11.6	33.1	32	4	US-08-647-924-20	Sequence 20, Appl
c 751	11.8	33.7	91	4	US-08-785-271-54	Sequence 54, Appl	c 824	11.6	33.1	33	4	US-09-069-781B-46	Sequence 46, Appl
c 752	11.8	33.7	94	5	PCR-US94-05150-36	Sequence 36, Appl	c 825	11.6	33.1	35	1	US-08-331-394-25	Sequence 25, Appl
c 753	11.8	33.7	96	1	US-08-053-131-142	Sequence 142, App	c 826	11.6	33.1	35	1	US-08-250-858-25	Sequence 25, Appl
c 754	11.8	33.7	96	1	US-08-645-641-142	Sequence 142, App	c 827	11.6	33.1	35	1	US-08-361-337-60	Sequence 60, Appl
c 755	11.8	33.7	96	1	US-07-853-408B-142	Sequence 142, App	c 828	11.6	33.1	35	1	US-08-446-915-25	Sequence 25, Appl
c 756	11.8	33.7	96	1	US-08-096-762-142	Sequence 142, App	c 829	11.6	33.1	35	2	US-08-744-139-25	Sequence 25, Appl
c 757	11.8	33.7	96	2	US-08-308-865-142	Sequence 142, App	c 830	11.6	33.1	35	3	US-08-435-568A-33	Sequence 33, Appl

831	11.6	33.1	35	5	PCT-US95-06639-25	Sequence 25, Appl	904	11.6	33.1	63	2	US-08-658-322-10	Sequence 10, Appl
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C 833	11.6	33.1	37	3	US-08-961-083-378	Sequence 378, App	906	11.6	33.1	63	2	US-08-757-531-66	Sequence 56, Appl
C 834	11.6	33.1	38	2	US-08-868-279-1	Sequence 1, Appl1	907	11.6	33.1	63	3	US-09-314-093-56	Sequence 56, Appl
835	11.6	33.1	40	1	US-08-137-117D-3	Sequence 3, Appl1	908	11.6	33.1	63	3	US-09-250-848-56	Sequence 56, Appl
836	11.6	33.1	40	1	US-08-436-717-3	Sequence 3, Appl1	909	11.6	33.1	63	4	US-09-251-885-56	Sequence 56, Appl
837	11.6	33.1	40	2	US-08-553-501A-3	Sequence 3, Appl1	910	11.6	33.1	63	4	US-09-337-635-56	Sequence 56, Appl
838	11.6	33.1	40	2	US-08-765-783A-3	Sequence 3, Appl1	911	11.6	33.1	64	2	US-08-658-322-4	Sequence 56, Appl1
839	11.6	33.1	40	3	US-08-921-100-3	Sequence 3, Appl1	912	11.6	33.1	64	2	US-08-658-322-5	Sequence 5, Appl1
840	11.6	33.1	40	3	US-08-880-142-3	Sequence 3, Appl1	913	11.6	33.1	64	2	US-08-658-322-6	Sequence 6, Appl1
841	11.6	33.1	40	3	US-08-902-201-3	Sequence 3, Appl1	914	11.6	33.1	64	2	US-08-658-322-7	Sequence 7, Appl1
842	11.6	33.1	40	3	US-08-933-983-24	Sequence 24, Appl1	C 915	11.6	33.1	64	2	US-08-821-782-1	Sequence 1, Appl1
843	11.6	33.1	40	3	US-09-205-231-3	Sequence 3, Appl1	C 916	11.6	33.1	64	3	US-08-881-094-29	Sequence 29, Appl1
844	11.6	33.1	40	3	US-09-277-016-20	Sequence 20, Appl1	C 917	11.6	33.1	64	4	US-09-292-435A-1	Sequence 1, Appl1
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846	11.6	33.1	40	4	US-09-416-557-3	Sequence 3, Appl1	C 919	11.6	33.1	65	1	US-08-146-886-20	Sequence 20, Appl1
C 847	11.6	33.1	41	2	US-08-053-451B-129	Sequence 129, App	C 920	11.6	33.1	69	4	US-09-109-613-30	Sequence 20, Appl1
C 848	11.6	33.1	41	4	US-09-039-982A-25	Sequence 25, Appl1	C 921	11.6	33.1	70	3	US-09-242-050-3	Sequence 20, Appl1
C 849	11.6	33.1	41	4	US-09-039-982A-26	Sequence 26, Appl1	C 922	11.6	33.1	71	4	US-09-364-902-8	Sequence 8, Appl1
C 850	11.6	33.1	41	4	US-09-039-641-25	Sequence 25, Appl1	C 923	11.6	33.1	75	3	US-09-182-859-31	Sequence 31, Appl1
851	11.6	33.1	41	4	US-09-039-641-26	Sequence 26, Appl1	C 924	11.6	33.1	77	1	US-07-982-712-8	Sequence 8, Appl1
C 852	11.6	33.1	41	4	US-09-039-762A-25	Sequence 25, Appl1	C 925	11.6	33.1	77	1	US-07-630-288A-37	Sequence 37, Appl1
853	11.6	33.1	41	4	US-09-039-762A-26	Sequence 26, Appl1	926	11.6	33.1	77	1	US-08-468-049-37	Sequence 37, Appl1
854	11.6	33.1	42	3	US-08-675-566-77	Sequence 77, Appl1	927	11.6	33.1	78	2	US-08-454-557C-70	Sequence 70, Appl1
C 855	11.6	33.1	43	4	US-09-079-431B-9	Sequence 9, Appl1	928	11.6	33.1	78	2	US-08-340-426D-70	Sequence 70, Appl1
C 856	11.6	33.1	44	1	US-08-290-311-12	Sequence 12, Appl1	929	11.6	33.1	78	2	US-08-450-673C-70	Sequence 70, Appl1
857	11.6	33.1	44	1	US-08-253-877C-44	Sequence 44, Appl1	C 930	11.6	33.1	78	3	US-08-955-568-40	Sequence 40, Appl1
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859	11.6	33.1	44	2	US-08-452-164A-44	Sequence 44, Appl1	932	11.6	33.1	78	5	PCT-US95-17111A-70	Sequence 40, Appl1
860	11.6	33.1	44	2	US-08-470-139-3	Sequence 3, Appl1	933	11.6	33.1	79	3	US-08-933-983-48	Sequence 48, Appl1
861	11.6	33.1	44	4	US-08-569-147-25	Sequence 25, Appl1	C 934	11.6	33.1	80	3	US-08-933-983-39	Sequence 39, Appl1
862	11.6	33.1	44	4	US-08-976-183A-20	Sequence 20, Appl1	C 935	11.6	33.1	80	3	US-08-933-983-57	Sequence 57, Appl1
863	11.6	33.1	44	4	US-09-347-061-3	Sequence 3, Appl1	C 936	11.6	33.1	81	1	US-07-764-466-1	Sequence 1, Appl1
864	11.6	33.1	45	1	US-07-756-251A-15	Sequence 15, Appl1	C 937	11.6	33.1	81	1	US-08-468-443-10	Sequence 10, Appl1
865	11.6	33.1	45	3	US-08-448-619-6	Sequence 6, Appl1	C 938	11.6	33.1	81	1	US-08-468-443-10	Sequence 10, Appl1
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C 868	11.6	33.1	47	2	US-08-487-113D-97	Sequence 97, Appl1	C 941	11.6	33.1	85	1	US-08-488-113B-145	Sequence 145, App
C 869	11.6	33.1	47	2	US-08-473-503-97	Sequence 97, Appl1	C 942	11.6	33.1	85	1	US-08-477-448B-145	Sequence 145, App
C 870	11.6	33.1	47	2	US-08-483-932-97	Sequence 97, Appl1	C 943	11.6	33.1	85	1	US-08-107-669D-37	Sequence 37, Appl1
C 871	11.6	33.1	47	2	US-08-720-420A-97	Sequence 97, Appl1	C 944	11.6	33.1	85	1	US-08-472-788A-37	Sequence 37, Appl1
C 872	11.6	33.1	47	3	US-08-714-017-97	Sequence 97, Appl1	C 945	11.6	33.1	85	1	US-08-477-531B-37	Sequence 37, Appl1
C 873	11.6	33.1	47	3	US-08-475-680-97	Sequence 97, Appl1	C 946	11.6	33.1	85	2	US-08-646-360-145	Sequence 145, App
C 874	11.6	33.1	47	3	US-09-338-907-211	Sequence 211, App	C 947	11.6	33.1	85	2	US-08-082-842A-37	Sequence 37, Appl1
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C 876	11.6	33.1	48	4	US-08-983-035A-53	Sequence 53, Appl1	C 949	11.6	33.1	85	3	US-09-136-389-145	Sequence 145, App
C 877	11.6	33.1	50	2	US-08-053-451B-136	Sequence 136, App	C 950	11.6	33.1	87	3	US-08-976-413A-308	Sequence 308, App
C 878	11.6	33.1	51	1	US-07-618-946B-14	Sequence 14, Appl1	C 951	11.6	33.1	87	4	US-09-364-539-125	Sequence 125, App
C 879	11.6	33.1	51	2	US-08-821-559A-14	Sequence 14, Appl1	952	11.6	33.1	88	2	US-08-497-124A-23	Sequence 23, Appl1
C 880	11.6	33.1	51	3	US-08-155-938-11	Sequence 11, Appl1	953	11.6	33.1	88	2	US-08-483-528B-85	Sequence 85, Appl1
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888	11.6	33.1	58	2	US-08-468-337-39	Sequence 39, Appl1	C 961	11.6	33.1	100	3	US-08-441-671-39	Sequence 29, Appl1
889	11.6	33.1	58	2	US-08-459-101A-6	Sequence 6, Appl1	C 962	11.6	33.1	100	3	US-08-441-971-30	Sequence 30, Appl1
C 890	11.6	33.1	59	2	US-08-308-887A-5	Sequence 5, Appl1	C 963	11.6	33.1	100	4	US-08-221-653-39	Sequence 29, Appl1
C 891	11.6	33.1	59	3	US-08-881-094-5	Sequence 5, Appl1	C 964	11.6	33.1	100	4	US-08-221-653-30	Sequence 29, Appl1
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893	11.6	33.1	60	1	US-08-484-192-177	Sequence 177, App	C 966	11.6	33.1	100	4	US-08-442-144A-20	Sequence 29, Appl1
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896	11.6	33.1	60	2	US-08-340-426D-58	Sequence 58, Appl1	969	11.4	32.6	17	4	US-08-584-040-7492	Sequence 7492, Ap
897	11.6	33.1	60	2	US-08-450-673C-58	Sequence 58, Appl1	C 970	11.4	32.6	18	4	US-09-214-178-6	Sequence 6, Appl1
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C 983 11.4 32.6 24 4 US-09-038-637-39 Sequence 39, Appl
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C 997 11.4 32.6 27 1 US-08-474-633A-14 Sequence 14, Appl
C 998 11.4 32.6 27 2 US-08-480-473B-8 Sequence 8, Appl
C 999 11.4 32.6 27 2 US-08-927-855-55 Sequence 55, Appl
C 1000 11.4 32.6 27 3 US-09-257-799-41 Sequence 41, Appl

ALIGNMENTS

RESULT 1
5196308-1/c
PATENT NO. 5196308
APPLICANT: NEPOM, GERALD T.; NEPOM, BARBARA S.
TITLE OF INVENTION: METHODS FOR IDENTIFYING THE DOW3.2
ALLELE ASSOCIATED WITH INCREASED RISK OF INSULIN-DEPENDENT
DIABETES MELLITUS
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/325,058
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Query Match 52.0%; Score 18.2; DB 6; Length 46;
Best Local Similarity 74.2%; Pred. No. 26;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 tgcctagatgggagatgggactctgac 33
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Db 34 tgcctgagatgggagatgctctgagc 4

RESULT 2
US-08-961-083-382/c
Sequence 382, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 382:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-083-382

Query Match 49.1%; Score 17.2; DB 3; Length 38;
Best Local Similarity 73.3%; Pred. No. 67;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 6 ctagaatgggagatgggactctgac 35
||||| | ||| | ||| |
Db 32 ctagaatgggagatgggactctgac 3

RESULT 3
US-08-086-428B-124/c
Sequence 124, Application US/08086428B
Patent No. 5514539
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NOCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-086-428B-124

Query Match 48.0%; Score 16.8; DB 1; Length 42;
Best Local Similarity 75.0%; Pred. No. 1e+02; 7; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 7;

Qy 1 catgtctagatgggagctgctc 28
||||| ||||| || ||||| |||||
Db 30 catgtctagatgggagctgctc 3

RESULT 4
US-08-468-570-124/C
Sequence 124, Application US/08468570
Patent No. 5871962

GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-570-124

Query Match 48.0%; Score 16.8; DB 2; Length 42;
Best Local Similarity 75.0%; Pred. No. 1e+02; 7; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 7;

Qy 1 catgtctagatgggagctgctc 28

Db 30 catgtctagatgggagctgctc 3
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RESULT 5
US-08-290-665A-228/C
Sequence 228, Application US/08290665A
Patent No. 5882852

GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ ID NO: 228:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-290-665A-228

Query Match 48.0%; Score 16.8; DB 2; Length 42;
Best Local Similarity 75.0%; Pred. No. 1e+02; 7; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 7;

Qy 1 catgtctagatgggagctgctc 28
||||| ||||| || ||||| |||||
Db 30 catgtctagatgggagctgctc 3

RESULT 6
PCT-US95-10398-228/C
Sequence 228, Application PC/TUS9510398
GENERAL INFORMATION:

APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN

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1 STREET: 345 PARK AVENUE
2 CITY: NEW YORK
3 STATE: NEW YORK
4 COUNTRY: USA
5 ZIP: 10154
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: FLOPPY DISK
9 COMPUTER: IBM PC COMPATIBLE
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: WORDPERFECT 5.1
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: PCT/US95/10398
15 FILING DATE: 15-AUG-1995
16 CLASSIFICATION:
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/086,428
20 FILING DATE: 29 JUNE 1993
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/290/665
24 FILING DATE: 15 AUGUST 1994
25
26 ATTORNEY/AGENT INFORMATION:
27 NAME: RICHARD W. BORK
28 REGISTRATION NUMBER: 36,459
29 REFERENCE/DOCKET NUMBER: 2026-4116
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (212) 751-4800
32 TELEFAX: (212) 751-6849
33
34 TELEX: 421792
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36 INFORMATION FOR SEQ ID NO: 228:
37
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 42 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
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44 PCT-US95-10398-228
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NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 00231/083001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-111-61

Query Match          45.1%; Score 15.8; DB 1; Length 75;
Best Local Similarity 65.7%; Pred. No.3e+02;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0

QY      1 catgtctgaatgggagatgggtcaactcgacct 35
        |||||  |||||  |||||  |||||  |||||
Dn      31 CACCTCAGCGCTGCGATGTCTGCTGGGCTGCACCT 65

RESULT      8
US-08-238-863-78
Sequence 78, Application US/08238863
Patent No. 5503978
GENERAL INFORMATION:
APPLICANT: SCHNEIDER, D. J., GOLD, L., AND FELIGON, J.
TITLE OF INVENTION: HIGH-AFFINITY SSDNA LIGANDS OF HIV-1
TITLE OF INVENTION: REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, Suite
         STREET: #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,863
FILING DATE: 6-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NX17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 81
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

```

US-08-238-863-78

Query Match 44.0%; Score 15.4; DB 1; Length 81;

Best Local Similarity 76.0%; Pred. No. 4.5e+02; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 6;

QY 3 tgcctagaatgggagtgagtcact 27
|||||
DB 35 tgcctagaatgggagtgagtcact 59

RESULT 9

US-08-443-407-78

Sequence 78, Application US/08443407

Patent No. 5786462

GENERAL INFORMATION:

APPLICANT: SCHNEIDER, D. J., GOLD, L., AND FEIGON, J.

TITLE OF INVENTION: HIGH-AFFINITY ssDNA

TITLE OF INVENTION: LIGANDS OF HIV-1 REVERSE

TITLE OF INVENTION: TRANSCRIPTASE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,407

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/238,863

FILING DATE: 6-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX17/C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 81

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-443-407-78

Query Match 44.0%; Score 15.4; DB 1; Length 81;

Best Local Similarity 76.0%; Pred. No. 4.5e+02;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 tgcctagaatgggagtgagtcact 27
|||||
DB 35 tgcctagaatgggagtgagtcact 59

RESULT 10

PCT-US95-05600-222

Sequence 222, Application PC/TUS9505600

GENERAL INFORMATION:

APPLICANT: GOLD, LARRY

APPLICANT: NIEWLANDT, DAN

APPLICANT: WECKER, MATTHEW

APPLICANT: SCHNEIDER, DANIEL J.

APPLICANT: FEIGON, JULI

APPLICANT: ALLEN, PATRICK

APPLICANT: SULLINGER, BRUCE A.

APPLICANT: DOUDNA, JENNIFER, A.

TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF

TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05600

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/238,863

FILING DATE: 06-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/248,632

FILING DATE: 24-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/303,362

FILING DATE: 09-SEPTEMBER-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/361,795

FILING DATE: 21-DECEMBER-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,991

FILING DATE: 08-SEPTEMBER-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

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APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

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APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

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APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

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FILING DATE: 11-JUNE-1990

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APPLICATION NUMBER: 07/714,131

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APPLICATION NUMBER: 07/536,428

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APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

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APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

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APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

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FILING DATE: 10-JUNE-1991

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APPLICATION NUMBER: 07/931,473

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PRIOR APPLICATION DATA:

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964

; INFORMATION FOR SEQ ID NO: 222:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 81 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 PCT-US93-05600-222

Query Match 44.0%; Score 15.4; DB 5; Length 81;
 Best local Similarity 76.0%; Pred. No. 4.5e+02;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 tgcctagaatgggagtgagctact 27
 Db 35 TGCTGAGAACTGGAAAGTGTCTACT 59

RESULT 11
 US-08-954-395A-28/C
 ; Sequence 28, Application US/08954395A
 ; Patent No. 6204022
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnson, Howard M.
 ; APPLICANT: Sudrmanlam, Prem S.
 ; APPLICANT: Pontzer, Carol H.
 ; APPLICANT: Villarete, Lorelle H.
 ; APPLICANT: Campos, Jackeline
 ; APPLICANT: Chung, Albert D.
 ; APPLICANT: Li, Wayne W.
 ; APPLICANT: Liu, Phillip T.
 ; TITLE OF INVENTION: LOW-TOXICITY HUMAN INTERFERON-ALPHA
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Dehlinger & Associates, LLP
 ; STREET: 350 Cambridge Ave., Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/954,395A
 ; FILING DATE: Filed Herewith
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/631,328
 ; FILING DATE: 12-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dehlinger, Peter J
 ; REGISTRATION NUMBER: 27008
 ; REFERENCE/DOCKET NUMBER: 5600-0001.35
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-324-0880
 ; TELEFAX: 650-324-0960
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 100 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: Frag N4, forward strand
 ; US-08-954-395A-28
 Query Match 44.0%; Score 15.4; DB 4; Length 100;

Best local Similarity 76.0%; Pred. No. 4.7e+02;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 11 atgggagtgagtgagctacttgacct 35
 Db 96 AAGAGATGGGGAATTCTGTGACAT 72

RESULT 12
 US-08-221-817-8
 ; Sequence 8, Application US/08221817
 ; Patent No. 532151
 ; GENERAL INFORMATION:
 ; APPLICANT: Chantry, David
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Hoekstra, Merle F.
 ; TITLE OF INVENTION: A No. 5532151el G Protein-coupled Receptor
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/221,817
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/123,932
 ; FILING DATE: 17 SEP 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5532151and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31981
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 32 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-221-817-8
 Query Match 42.9%; Score 15; DB 1; Length 32;
 Best local Similarity 78.3%; Pred. No. 5.6e+02;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 atgtctagaatgggagtgagtc 24
 Db 1 ATTTCTAGAAATGGGACGTGGCC 23
 RESULT 13
 US-08-454-439-8
 ; Sequence 8, Application US/08454439
 ; Patent No. 5591618
 ; GENERAL INFORMATION:
 ; APPLICANT: Chantry, David
 ; APPLICANT: Gray, Patrick W.

APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5591618and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-454-439-8

Query Match 42.9%; Score 15; DB 1; Length 32;
Best Local Similarity 78.3%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 atgtctagaatgctggatggtc 24
|||
Db 1 ATTCTAGATGCGAGCTGGCC 23

RESULT 14
PCT-US94-10487-8
Sequence 8, Application PC/TUS9410487
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10487
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,817
FILING DATE: 31 MAR 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US94-10487-8

Query Match 42.9%; Score 15; DB 5; Length 32;
Best Local Similarity 78.3%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 atgtctagaatgctggatggtc 24
|||
Db 1 ATTCTAGATGCGAGCTGGCC 23

RESULT 15
US-07-665-960A-10
Sequence 10, Application US/07665960A
Patent No. 5578443
GENERAL INFORMATION:
APPLICANT: Santamaria, Pedro
APPLICANT: Boyce-Jacino, Michael T.
APPLICANT: Barbosa, Jose J.
APPLICANT: Rich, Stephen S.
APPLICANT: Faras, Anthony J.
TITLE OF INVENTION: DNA Sequence-Based HLA Typing
TITLE OF INVENTION: Method
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 NO. 5578443west Center
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb.
COMPUTER: NO. 5578443ingate 386
OPERATING SYSTEM: DOS 4.0
SOFTWARE: WordPerfect-5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/665,960A
FILING DATE: 19910306
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kowalczyk, Alan W.
REGISTRATION NUMBER: 31,535

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; REFERENCE/DOCKET NUMBER: 600.190-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 332-5300
; TELEFAX: (612) 332-9081
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Genomic DNA
; ANTI-SENSE: yes
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
; NAME/KEY: Oligonucleotide Primer DOB30
; LOCATION: Anneals to codons 97 to 104 of the
; LOCATION: DOB1 transcript of HLA class II
US-07-665-960A-10

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Query Match      41.7%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      11 atgggagatgggtcactctgg 31
         |||||  |||||  |||
Db       1 ATGGGAGATGTCACCTGTGG 21

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Search completed: June 22, 2002, 05:33:43
Job time: 4753 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 04:59:26 ; Search time 2443.9 Seconds
(Without alignments)
193.295 Million cell updates/sec

Title: US-09-927-267-13
Perfect score: 35
Sequence: 1 catgtctagatcgggagatggtcactctgacact 35

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues
Total number of hits satisfying chosen parameters: 297742

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
EST: *
1: em_estba: *
2: em_esthm: *
3: em_estin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_estl: *
10: gb_est2: *
11: gb_hlc: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pln: *
16: em_gss_vrc: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	53.1	38	12	A2773847
2	17.4	49.7	79	9	AA668503
3	17.4	49.7	79	9	AA954823
4	17.4	49.7	79	9	AA1082539
5	17.4	49.7	79	9	AA1085281
6	17.4	49.7	79	9	AA142830
7	17.4	49.7	79	9	AA1675555
8	17.4	49.7	79	9	AA620456
9	17.4	49.7	85	10	W20254
10	16.6	47.4	60	12	B39007
11	16.6	47.4	100	9	AA429430
12	16.6	46.9	100	9	AA366936
13	16.2	46.3	79	9	AA723716
14	16.2	46.3	81	9	AA166006
15	16.2	45.7	58	9	AA960093
16	16.2	45.7	62	9	AA405653
17	16.2	45.7	79	9	AA107824

18	16	45.7	89	9	AM197197	AM197197 xm38a06.x
19	16	45.7	100	9	AA286603	AA286603 vb78a03.r
20	15.8	45.1	56	12	A2767267	A2767267 IM0566A23
21	15.8	45.1	59	12	BH011505	BH011505 BG02443-5
22	15.8	45.1	81	9	AA775436	AA775436 ad13f09.s
23	15.8	45.1	81	9	AA994005	AA994005 ou42c02.s
24	15.6	44.6	63	12	A2921625	A2921625 1006030G0
25	15.6	44.6	77	10	N44726	N44726 yv37c09.r1
26	15.6	44.6	80	12	A2921665	A2921665 1006031B0
27	15.6	44.6	90	10	BI791330	BI791330 1004f05.y
28	15.6	44.6	96	10	T97453	T97453 y57h06.r1
29	15.6	44.6	100	9	AA929885	AA929885 vz44d11.r
30	15.4	44.0	40	9	AA921997	AA921997 om14a10.s
31	15.4	44.0	64	12	HSWC13F04	HSWC13F04 H.sepiens D
32	15.4	44.0	70	9	A1032382	A1032382 cv37e10.x
33	15.4	44.0	70	10	F30991	F30991 HSPD21806.H
34	15.4	44.0	71	10	BI557731	BI557731 603237092
35	15.4	44.0	80	10	BG061881	BG061881 L0952H02-
36	15.4	44.0	81	9	AA464680	AA464680 zx85f06.r
37	15.4	44.0	83	12	A2918804	A2918804 1006008D1
38	15.4	44.0	87	9	A1859974	A1859974 wm22c08.x
39	15.4	44.0	94	9	AA960499	AA960499 vw63e07.s
40	15.4	44.0	100	9	AA907309	AA907309 s155d01.y
41	15.2	43.4	24	12	A2346754	A2346754 IM0082E12
42	15.2	43.4	57	12	B02157	B02157 CSRL-149A11
43	15.2	43.4	79	10	BG272579	BG272579 nah28a06.
44	15.2	43.4	82	10	R06472	R06472 yf09a05.r1
45	15.2	43.4	85	9	AA451958	AA451958 zx12d12.r
46	15.2	43.4	98	12	A2357824	A2357824 IM0099J08
47	15.2	42.9	49	9	A1383078	A1383078 lc20h09.x
48	15.2	42.9	50	12	A2794281	A2794281 IM0066C04
49	15.2	42.9	57	12	A2336153	A2336153 2M0048B04
50	15.2	42.9	80	12	TA36H07P	TA36H07P T. brucei
51	15.2	42.9	86	10	R29008	R29008 F0-76D 22 W
52	15.2	42.9	89	12	TA36H07Q	TA36H07Q T. brucei
53	15.2	42.9	93	9	AA692582	AA692582 vc61a08.r
54	15.2	42.9	96	9	AA090390	AA090390 xc81e12.x
55	15.2	42.9	99	12	A2512819	A2512819 IM0358I07
56	14.8	42.3	40	9	AA247854	AA247854 2820389.3
57	14.8	42.3	56	10	BI791026	BI791026 1004f05.x
58	14.8	42.3	57	12	A2774746	A2774746 2M0004B04
59	14.8	42.3	60	12	A2759519	A2759519 IM0552G08
60	14.8	42.3	77	10	W58820	W58820 md44b11.r1
61	14.8	42.3	78	9	A1142416	A1142416 q96f1f06.s
62	14.8	42.3	81	9	AA903760	AA903760 ok66e05.s
63	14.8	42.3	83	12	A2381974	A2381974 IM0138F15
64	14.8	42.3	98	9	A1174454	A1174454 an46e03.s
65	14.6	41.7	34	12	A2818088	A2818088 2M0087I21
66	14.6	41.7	47	12	A2444521	A2444521 IM0239F13
67	14.6	41.7	52	9	A1397068	A1397068 fb25h05.y
68	14.6	41.7	52	12	A2843674	A2843674 2M0142G08
69	14.6	41.7	58	9	A1720114	A1720114 as78f06.x
70	14.6	41.7	59	10	T24794	T24794 EST369 Huma
71	14.6	41.7	61	9	A1954288	A1954288 wx95d12.x
72	14.6	41.7	67	9	AA907371	AA907371 OJ70h02.s
73	14.6	41.7	77	12	A2468774	A2468774 IM0281O18
74	14.6	41.7	79	9	A1018118	A1018118 ct91f06.s
75	14.6	41.7	83	9	AA647456	AA647456 vq82d12.s
76	14.6	41.7	87	9	AA243934	AA243934 mx95f08.r
77	14.6	41.7	88	9	A1866758	A1866758 tz25e10.x
78	14.6	41.7	89	9	A1656448	A1656448 ct45h01.x
79	14.6	41.7	91	10	BG142577	BG142577 1689D02.Y
80	14.6	41.7	97	10	BM122580	BM122580 L0512B07-
81	14.4	41.1	43	9	A1283683	A1283683 q172g11.x
82	14.4	41.1	50	9	AU105373	AU105373 AU105373
83	14.4	41.1	55	9	A1965095	A1965095 fc86g04.y
84	14.4	41.1	63	12	A2941669	A2941669 2M0201F04
85	14.4	41.1	67	9	A1791108	A1791108 uk55g10.Y
86	14.4	41.1	67	9	AA161388	AA161388 q939f12.s
87	14.4	41.1	70	9	A1969665	A1969665 wq78e01.x
88	14.4	41.1	79	10	H55371	H55371 CHR220310.C
89	14.4	41.1	82	9	AF211796	AF211796 AF211796
90	14.4	41.1	82	12	A2443108	A2443108 IM0237F07

C 91	14.4	41.1	83	10	BE532471	BE532471 601233840	164	13.8	39.4	76	9	AA574786	AA574786 vm29g01.r
C 92	14.4	41.1	86	10	R55300	R55300 yj77e04.s1	C 165	13.8	39.4	79	9	AA082217	AA082217 zn37e02.r
C 93	14.4	41.1	89	12	AZ921213	AZ921213 1006024H0	C 166	13.8	39.4	79	10	T48702	T48702 ypd1909.s1
C 94	14.4	41.1	92	10	T65323	T65323 yc79h10.s1	C 167	13.8	39.4	82	10	B1156080	B1156080 602903639
C 95	14.4	41.1	94	9	A1049059	A1049059 ub39g04.r	C 168	13.8	39.4	82	10	BM142397	BM142397 if35h10.y
C 96	14.4	41.1	95	10	R71404	R71404 y180h08.s1	C 169	13.8	39.4	82	10	N34487	N34487 yy13g06.s1
C 97	14.4	41.1	98	12	AZ793766	AZ793766 2M0047F08	C 170	13.8	39.4	85	9	AA918440	AA918440 om38a11.s
C 98	14.4	41.1	100	9	AA490921	AA490921 aa52d04.s	C 171	13.8	39.4	87	9	AA460203	AA460203 sh56c09.y
C 99	14.4	41.1	100	10	BF171367	BF171367 PCL2547 M	C 172	13.8	39.4	89	9	AA948523	AA948523 cn59e09.s
C 100	14.2	40.6	60	12	AZ447238	AZ447238 1M0244M15	C 173	13.8	39.4	89	9	AA63746	AA63746 vq69g09.s
C 101	14.2	40.6	60	12	AZ917918	AZ917918 1006002E1	C 174	13.8	39.4	91	9	AA222071	AA222071 mw73h03.r
C 102	14.2	40.6	63	12	AZ307924	AZ307924 1M0010E24	C 175	13.8	39.4	92	9	A1538099	A1538099 co19c01.x
C 103	14.2	40.6	70	9	AA908439	AA908439 og78f02.s	C 176	13.8	39.4	93	10	T61441	T61441 yc06c12.s1
C 104	14.2	40.6	70	9	AA985157	AA985157 am75f07.s	C 177	13.8	39.4	93	12	AZ811283	AZ811283 2M0077B17
C 105	14.2	40.6	73	9	A1823606	A1823606 w171c01.x	C 178	13.8	39.4	94	9	A1969558	A1969558 wz68b05.x
C 106	14.2	40.6	79	10	H37875	H37875 yp57f03.r1	C 179	13.8	39.4	97	9	A1855642	A1855642 sc32a10.y
C 107	14.2	40.6	80	9	AA814066	AA814066 ob90f11.s	C 180	13.8	39.4	98	9	A1472650	A1472650 tj93h11.x
C 108	14.2	40.6	82	9	AA145585	AA145585 mt63a02.r	C 181	13.8	39.4	100	9	AA847608	AA847608 ce19e02.s
C 109	14.2	40.6	83	9	A1537820	A1537820 tp35g11.x	C 182	13.8	39.4	100	9	AA897598	AA897598 oj77f03.s
C 110	14.2	40.6	85	9	AA472980	AA472980 vb31g12.r	C 183	13.8	39.4	100	9	A1768071	A1768071 w146d12.x
C 111	14.2	40.6	87	9	AA760429	AA760429 vv77a01.r	C 184	13.8	39.4	100	9	BG955738	BG955738 CM4-CT065
C 112	14.2	40.6	87	10	BF233565	BF233565 602024172	C 185	13.6	38.9	43	9	AA423162	AA423162 ve36b01.r
C 113	14.2	40.6	87	12	AZ807995	AZ807995 2M0071D16	C 186	13.6	38.9	45	12	TA67D110	TA67D110 T.brucet
C 114	14.2	40.6	88	9	AA780283	AA780283 af55f10.s	C 187	13.6	38.9	49	9	AA947544	AA947544 od87b10.s
C 115	14.2	40.6	94	9	AA904344	AA904344 o115a05.s	C 188	13.6	38.9	50	12	AZ834614	AZ834614 2M0117121
C 116	14.2	40.6	94	9	A1805581	A1805581 tx86h05.x	C 189	13.6	38.9	51	12	AZ606792	AZ606792 1M0428G23
C 117	14.2	40.6	94	12	AZ763838	AZ763838 1M0559B03	C 190	13.6	38.9	55	9	AA581159	AA581159 nd14f07.r
C 118	14.2	40.6	97	9	AAW567085	AAW567085 FK32h11.x	C 191	13.6	38.9	61	9	AA756797	AA756797 vv72b01.r
C 119	14.2	40.6	97	12	AZ327132	AZ327132 1M0050M13	C 192	13.6	38.9	61	12	AZ442540	AZ442540 1M0236011
C 120	14.2	40.6	99	12	AZ473085	AZ473085 1M0288F16	C 193	13.6	38.9	61	12	AZ502948	AZ502948 1M0342B06
C 121	14.2	40.6	100	9	AA773496	AA773496 af77g06.r	C 194	13.6	38.9	61	12	AZ502948	AZ502948 1M0342B06
C 122	14.2	40.6	100	9	BE184989	BE184989 MRL-HT070	C 195	13.6	38.9	67	12	HSKC45F02	HSKC45F02 H.sapiens D
C 123	14	40.0	53	9	A1020994	A1020994 ua98e01.r	C 196	13.6	38.9	70	10	N23321	N23321 vx78e12.s1
C 124	14	40.0	58	9	AA434042	AA434042 zw24D05.r	C 197	13.6	38.9	71	9	AA791688	AA791688 vs64a07.r
C 125	14	40.0	59	10	BJ060535	BJ060535 BJO60535	C 198	13.6	38.9	71	9	A1784010	A1784010 co29a04.x
C 126	14	40.0	60	10	BE778580	BE778580 601466112	C 199	13.6	38.9	72	10	U25930	U25930 HSU25930 Hu
C 127	14	40.0	67	9	A1223841	A1223841 q133f02.x	C 200	13.6	38.9	73	10	BE400544	BE400544 SMOV13CAN
C 128	14	40.0	70	9	A1530845	A1530845 tx53h04.x	C 201	13.6	38.9	75	12	AZ496458	AZ496458 1M0332G23
C 129	14	40.0	70	9	A1702226	A1702226 we04a03.x	C 202	13.6	38.9	76	9	AA237521	AA237521 mx15a06.r
C 130	14	40.0	72	10	R81163	R81163 y121d12.s3	C 203	13.6	38.9	76	12	AZ979161	AZ979161 2M0255E17
C 131	14	40.0	78	10	BF971045	BF971045 602270381	C 204	13.6	38.9	79	9	AA192941	AA192941 zq13c07.s
C 132	14	40.0	78	10	B1851925	B1851925 6043h12.s4	C 205	13.6	38.9	81	10	T68183	T68183 yc40g05.s1
C 133	14	40.0	79	9	AA910138	AA910138 og04h12.s	C 206	13.6	38.9	83	9	AA302066	AA302066 xrf3a02.x
C 134	14	40.0	79	9	AA934942	AA934942 ny33b08.s	C 207	13.6	38.9	89	9	AA742627	AA742627 ny90e02.s
C 135	14	40.0	79	9	AU076877	AU076877 AU076877	C 208	13.6	38.9	90	9	AAW073015	AAW073015 xa61d01.x
C 136	14	40.0	83	9	AV854495	AV854495 AV854495	C 209	13.6	38.9	90	9	AAW274327	AAW274327 xs74c11.x
C 137	14	40.0	84	12	AZ315745	AZ315745 1M0033A05	C 210	13.6	38.9	93	10	BE857752	BE857752 7d61a09.x
C 138	14	40.0	84	12	AZ392796	AZ392796 1M0155N06	C 211	13.6	38.9	93	9	AAW249746	AAW249746 2819789.3
C 139	14	40.0	85	10	BG063866	BG063866 H3011F09-	C 212	13.6	38.9	93	9	BE049038	BE049038 xrf6s12.x
C 140	14	40.0	86	9	AA895383	AA895383 yv33e10.r	C 213	13.6	38.9	94	9	AAW48374	AAW48374 oa53h07.s
C 141	14	40.0	87	12	AF191711	AF191711 AF191711	C 214	13.6	38.9	94	9	AAW072716	AAW072716 xa59c05.x
C 142	14	40.0	88	9	AA839016	AA839016 vw93a05.r	C 215	13.6	38.9	95	9	A1318466	A1318466 ta80h09.x
C 143	14	40.0	89	10	BG108678	BG108678 HRPE0031	C 216	13.6	38.9	95	10	N92836	N92836 zb67f05.s1
C 144	14	40.0	89	10	H13155	H13155 yj16b07.s1	C 217	13.6	38.9	97	10	R85074	R85074 yd04f12.r1
C 145	14	40.0	90	12	AZ395149	AZ395149 1M0159G01	C 218	13.6	38.9	97	12	AF088136	AF088136 AF088136
C 146	14	40.0	93	10	BE680398	BE680398 602154186	C 219	13.6	38.9	97	12	AZ565834	AZ565834 214PvA04
C 147	14	40.0	96	9	AAW830718	AAW830718 sm35d03.y	C 220	13.6	38.9	98	9	AAW11302	AAW11302 sg35b11.y
C 148	14	40.0	96	10	BF725570	BF725570 bx18a12.x	C 221	13.6	38.9	98	12	AZ610213	AZ610213 1M0435F50
C 149	14	40.0	97	9	AA234884	AA234884 zr77h01.r	C 222	13.6	38.9	99	9	AAW78104	AAW78104 op32b04.s
C 150	14	40.0	98	12	CNS04C2M	CNS04C2M Tetraodon	C 223	13.6	38.9	99	10	H99013	H99013 yy11c09.r1
C 151	14	40.0	99	9	AA511790	AA511790 vg16f08.r	C 224	13.6	38.9	99	12	AZ632440	AZ632440 1M0107J02
C 152	14	40.0	100	9	A1834244	A1834244 uc0-HT001	C 225	13.6	38.9	99	12	BH407959	BH407959 1007053F0
C 153	14	40.0	100	9	AAW13579	AAW13579 ro37b03.x	C 226	13.6	38.9	100	9	AA995347	AA995347 os09g08.s
C 154	14	40.0	100	9	AAW52355	AAW52355 RC2-CT020	C 227	13.6	38.9	100	9	AAW388445	AAW388445 MR2-ST012
C 155	13.8	39.4	34	9	A1721161	A1721161 as73h12.x	C 228	13.6	38.9	100	9	AAW842768	AAW842768 MR2-CN003
C 156	13.8	39.4	40	9	A1123110	A1123110 qa85c06.s	C 229	13.6	38.9	100	10	BG213902	BG213902 RST33525
C 157	13.8	39.4	46	12	AAZ59692	AAZ59692 1M0410P04	C 230	13.6	38.9	100	10	BG249248	BG249248 603361691
C 158	13.8	39.4	47	12	AAZ824937	AAZ824937 2M0095A24	C 231	13.6	38.9	100	10	BE483805	BE483805 170124 BA
C 159	13.8	39.4	54	9	A1132037	A1132037 vG82h05.r	C 232	13.4	38.3	34	12	AZ819940	AZ819940 2M0091D19
C 160	13.8	39.4	54	9	A1119329	A1119329 mp80d09.r	C 233	13.4	38.3	39	9	AAV852693	AAV852693 AV852693
C 161	13.8	39.4	64	10	B1142414	B1142414 SMOv3CMC	C 234	13.4	38.3	39	12	AZ391588	AZ391588 1M0153K18
C 162	13.8	39.4	75	9	A1918210	A1918210 tD06f01.x	C 235	13.4	38.3	40	10	BG431777	BG431777 602499587
C 163	13.8	39.4	75	12	CNS03YFO	AL266553 Tetraodon	C 236	13.4	38.3	44	10	AZ649612	AZ649612 1M0519H17

237	13.4	38.3	55	12	TA121A10P	AL465712 T. bruce1	c 310	13.2	37.7	69	9	AI588687	AI588687 fb98c01.y
238	13.4	38.3	58	10	R76020	R76020 y122q10.s1	c 311	13.2	37.7	70	9	AA460112	AA460112 zxb8e03.r
239	13.4	38.3	61	9	AI735643	AI735643 at19a05.x	c 312	13.2	37.7	71	12	AZ816914	AZ816914 2M0085C21
240	13.4	38.3	63	10	B1048110	B1048110 B1048110	c 313	13.2	37.7	71	12	TA9C01P	TA9C01P T. bruce1
241	13.4	38.3	65	9	AM695641	AM695641 NF097C06S	c 314	13.2	37.7	73	10	BF400540	BF400540 SMOVL3CAN
242	13.4	38.3	65	12	BH415614	BH415614 1007043HO	c 315	13.2	37.7	73	12	AZ919172	AZ919172 1006014C0
243	13.4	38.3	67	10	R71808	R71808 yJ86b01.r1	c 316	13.2	37.7	75	9	AA606357	AA606357 v047f09.r
244	13.4	38.3	69	12	CNS02XRS	AL128714 Tetradon	c 317	13.2	37.7	76	10	D43333	D43333 D43333 R1CE
245	13.4	38.3	71	9	AA966926	AA966926 ua38a07.r	c 318	13.2	37.7	78	9	AA746106	AA746106 nv94af02.s
246	13.4	38.3	71	10	B1557812	B1557812 603236992	c 319	13.2	37.7	78	10	D82266	D82266 H0MBC4231
247	13.4	38.3	72	10	U44175	U44175 EN044175 As	c 320	13.2	37.7	81	9	AV565298	AV565298 AV565298
248	13.4	38.3	72	10	BF021521	BF021521 uy48b10.y	c 321	13.2	37.7	83	9	AA921081	AA921081 vy84q11.r
249	13.4	38.3	72	10	BF03125	BF03125 601454547	c 322	13.2	37.7	84	9	AI725315	AI725315 1181 P1F
250	13.4	38.3	73	9	AA976253	AA976253 oc03f04.s	c 323	13.2	37.7	84	10	BG169944	BG169944 602321649
251	13.4	38.3	73	9	AI160767	AI160767 qb53f06.x	c 324	13.2	37.7	85	9	AA810795	AA810795 ob66b09.s
252	13.4	38.3	74	12	AZ330761	AZ330761 1M0056L10	c 325	13.2	37.7	85	9	AI477019	AI477019 fb54f01.x
253	13.4	38.3	76	9	AI182038	AI182038 ud73c07.y	c 326	13.2	37.7	85	10	BG815145	BG815145 dac01e11.
254	13.4	38.3	77	9	AI655605	AI655605 ts99c07.x	c 327	13.2	37.7	86	9	AA666896	AA666896 v185h03.s
255	13.4	38.3	77	12	AZ483071	AZ483071 1M0308F05	c 328	13.2	37.7	87	12	AZ836319	AZ836319 1M0141P13
256	13.4	38.3	78	12	AZ513591	AZ513591 1M0359D11	c 329	13.2	37.7	87	12	AZ807295	AZ807295 2M0070K01
257	13.4	38.3	79	9	AA764740	AA764740 n263d05.s	c 330	13.2	37.7	88	12	AZ438919	AZ438919 1M0229PF17
258	13.4	38.3	79	9	AA421588	AA421588 zuz25e02.r	c 331	13.2	37.7	89	9	AI493950	AI493950 qz52a03.x
259	13.4	38.3	79	10	BF140210	BF140210 601786792	c 332	13.2	37.7	89	10	BI192026	BI192026 14d12fs..f
260	13.4	38.3	79	10	BF147359	BF147359 us30e02.x	c 333	13.2	37.7	91	9	AI331553	AI331553 fa94c02.y
261	13.4	38.3	80	12	AZ417201	AZ417201 1M0192H16	c 334	13.2	37.7	91	10	R50465	R50465 yJ56f12..r1
262	13.4	38.3	81	12	AZ508498	AZ508498 1M0350J24	c 335	13.2	37.7	93	12	AZ805947	AZ805947 2M0185PF17
263	13.4	38.3	82	9	AA676707	AA676707 z364d04.s	c 336	13.2	37.7	93	12	AZ872079	AZ872079 2M0185PF17
264	13.4	38.3	83	9	AA429536	AA429536 zw74c11.r	c 337	13.2	37.7	93	12	BH227263	BH227263 1006138E0
265	13.4	38.3	83	12	AZ580213	AZ580213 1M0368C21	c 338	13.2	37.7	94	9	AI234364	AI234364 qh82f10.x
266	13.4	38.3	83	12	AZ774496	AZ774496 2M0004G02	c 339	13.2	37.7	94	9	AA074184	AA074184 t82d06.r
267	13.4	38.3	85	9	BE223013	BE223013 hu46a04.x	c 340	13.2	37.7	95	12	AZ648429	AZ648429 1M0517N19
268	13.4	38.3	85	12	AZ774997	AZ774997 2M0004G24	c 341	13.2	37.7	97	10	R60419	R60419 yH08a02..r1
269	13.4	38.3	87	12	AZ807295	AZ807295 2M0070K01	c 342	13.2	37.7	98	12	AI2916596	AI2916596 Pet1.7.h6
270	13.4	38.3	88	9	AV837986	AV837986 AV837986	c 343	13.2	37.7	99	9	AI006397	AI006397 AT006397
271	13.4	38.3	88	10	B1029074	B1029074 B1029074	c 344	13.2	37.7	99	9	AM053901	AM053901 50..comp15
272	13.4	38.3	88	12	AF219064	AF219064 AF219064	c 345	13.2	37.7	100	9	AM620205	AM620205 s193b06.y
273	13.4	38.3	89	10	N20346	N20346 yx38f01.s1	c 346	13.2	37.7	100	10	BF801248	BF801248 QV4-C1010
274	13.4	38.3	90	9	AA923319	AA923319 o144b05.s	c 347	13.2	37.7	100	10	BF539034	BF539034 602048583
275	13.4	38.3	90	10	BG405953	BG405953 s8c40b04.	c 348	13.2	37.7	100	12	AZ465644	AZ465644 1M0275003
276	13.4	38.3	91	9	AI196205	AI196205 u170c05.y	c 349	13	37.1	27	12	AZ784820	AZ784820 2M0028N04
277	13.4	38.3	91	10	T64061	T64061 yc05c10.r1	c 350	13	37.1	31	10	BE356410	BE356410 601064417
278	13.4	38.3	91	10	BE334223	BE334223 us30e02.y	c 351	13	37.1	31	12	AZ995788	AZ995788 2M0281D15
279	13.4	38.3	92	10	HS011941	HS011941 Homo sapi	c 352	13	37.1	33	12	AZ444218	AZ444218 1M0239N07
280	13.4	38.3	92	10	HS5123	HS5123 CHR220062.C	c 353	13	37.1	36	12	AZ839832	AZ839832 2M0136D12
281	13.4	38.3	94	12	BH2232319	BH2232319 1006106E1	c 354	13	37.1	37	10	BM395102	BM395102 50072.-2-7
282	13.4	38.3	95	9	AA681827	AA681827 vu75a01.r	c 355	13	37.1	38	12	BH129371	BH129371 G-5b8.f.M
283	13.4	38.3	95	9	AA930834	AA930834 my55e05.r	c 356	13	37.1	39	12	AZ862168	AZ862168 2M0169C18
284	13.4	38.3	95	10	BG076487	BG076487 H3003B06-	c 357	13	37.1	40	12	AZ371110	AZ371110 1M0122105
285	13.4	38.3	95	12	AZ514788	AZ514788 1M0361A17	c 358	13	37.1	43	9	AI437739	AI437739 sa39a01.y
286	13.4	38.3	96	12	AZ423192	AZ423192 1M0202M07	c 359	13	37.1	47	12	AZ474499	AZ474499 1M0292E07
287	13.4	38.3	97	10	T81216	T81216 yd96g08.r1	c 360	13	37.1	49	9	AA937018	AA937018 o172a04.s
288	13.4	38.3	98	10	H59870	H59870 yrl13h05.s1	c 361	13	37.1	50	9	AI0107408	AI0107408 AI0107408
289	13.4	38.3	100	9	AL649251	AL649251 AL649251	c 362	13	37.1	50	9	AI0107595	AI0107595 AI0107595
290	13.4	38.3	100	9	AM370035	AM370035 RC6-BF024	c 363	13	37.1	50	9	AI0107601	AI0107601 AI0107601
291	13.4	38.3	100	10	BG910769	BG910769 602810458	c 364	13	37.1	51	12	B36265	B36265 HS-1038-A2-
292	13.4	37.7	36	12	AZ817178	AZ817178 2M0086C21	c 365	13	37.1	51	12	B36265	B36265 HS-1038-A2-
293	13.2	37.7	46	9	AA796136	AA796136 vp18a03.r	c 366	13	37.1	52	9	AA989017	AA989017 cr82d03.s
294	13.2	37.7	49	9	AI269199	AI269199 qf68f01.x	c 367	13	37.1	52	9	AI471332	AI471332 tm09h11.x
295	13.2	37.7	50	9	AI819158	AI819158 wJ94c07.x	c 368	13	37.1	52	10	BF63970	BF63970 NF028G041
296	13.2	37.7	50	9	AI0106800	AI0106800 AI0106800	c 369	13	37.1	54	12	AZ918633	AZ918633 1006004H0
297	13.2	37.7	53	9	AA020567	AA020567 m61d11.r	c 370	13	37.1	58	9	AI940991	AI940991 sP82h08.y
298	13.2	37.7	55	12	AZ345660	AZ345660 1M0080M24	c 371	13	37.1	58	12	BH219485	BH219485 1006087G0
299	13.2	37.7	55	12	AZ345660	AZ345660 1M0080M24	c 372	13	37.1	61	10	BG099116	BG099116 n8g46h01.
300	13.2	37.7	57	12	BH230444	BH230444 1006158A0	c 373	13	37.1	63	9	AA705649	AA705649 zF40c06.s
301	13.2	37.7	58	12	AA002320	AA002320 m942h05.r	c 374	13	37.1	64	9	AI005788	AI005788 ua82h04.r
302	13.2	37.7	58	12	GGA320139	AJ2320243 Gal1us ga	c 375	13	37.1	64	9	AA158881	AA158881 z056d12.r
303	13.2	37.7	61	12	AZ840071	AZ840071 2M0136N22	c 376	13	37.1	64	12	BH622818	BH622818 1007098H0
304	13.2	37.7	62	12	AZ800802	AZ800802 2M0059F05	c 377	13	37.1	66	12	AZ400381	AZ400381 1M0166G08
305	13.2	37.7	64	10	BE636276	BE636276 SMOVAMCA0	c 378	13	37.1	72	12	AZ312454	AZ312454 1M0028K18
306	13.2	37.7	65	12	AZ665658	AZ665658 1M0548K15	c 379	13	37.1	72	12	TA42H10Q	TA42H10Q AI194077
307	13.2	37.7	65	12	BH218101	BH218101 1006074F1	c 380	13	37.1	73	9	AA194077	AA194077 z137d01.s
308	13.2	37.7	67	9	AI901117	AI901117 sc19h05.y	c 381	13	37.1	73	12	BH619818	BH619818 1007063A0
309	13.2	37.7	67	10	H39403	H39403 DR95 IFNGm	c 382	13	37.1	73	12	TA253A04P	TA253A04P AI463613 T. bruce1

C 383	13	37.1	76	9	A1748627	C 456	12.8	36.6	67	12	A2508991	A2508991	1M0351A14
C 384	13	37.1	77	12	A2633034	457	12.8	36.6	67	12	TAI62F060	AI472284	T. brucei
C 385	13	37.1	78	12	A2801938	458	12.8	36.6	68	12	A2822259	A2822259	2M0095M13
C 386	13	37.1	79	12	A2918536	C 459	12.8	36.6	73	10	F28512	F28512	HSPD17644
C 387	13	37.1	79	9	AA886266	460	12.8	36.6	74	10	D21007	D21007	HSPD501989
C 388	13	37.1	79	9	AA190950	461	12.8	36.6	75	9	AA144884	AA144884	mt11D08.r
C 389	13	37.1	81	9	AU055641	C 462	12.8	36.6	75	10	BI916780	BI916780	60317878
C 390	13	37.1	82	9	AA913406	463	12.8	36.6	75	10	H41220	H41220	Y664112.s1
C 391	13	37.1	82	9	AA916958	464	12.8	36.6	76	10	R53414	R53414	Y1701E06.r
C 392	13	37.1	82	9	AA987833	C 465	12.8	36.6	78	9	AA436198	AA436198	z22E09.s
C 393	13	37.1	82	12	A2784268	466	12.8	36.6	80	10	AA36198	AA36198	602336678
C 394	13	37.1	83	12	A2514475	467	12.8	36.6	81	12	BG173107	BG173107	602336678
C 395	13	37.1	83	12	BH224287	C 468	12.8	36.6	82	9	A2634225	A2634225	1007078D1
C 396	13	37.1	84	12	AA272792	C 469	12.8	36.6	82	9	AA813666	AA813666	a169405.s
C 397	13	37.1	84	12	A2609829	C 470	12.8	36.6	82	9	AA653374	AA653374	AL653374
C 398	13	37.1	85	9	AA124662	C 471	12.8	36.6	83	9	A1624949	A1624949	ts48c10.x
C 399	13	37.1	85	9	AA194691	C 472	12.8	36.6	83	12	A2514421	A2514421	1M0361005
C 400	13	37.1	86	10	BI324530	473	12.8	36.6	83	12	A2953673	A2953673	2M0219H01
C 401	13	37.1	86	10	T11175	474	12.8	36.6	84	9	AI458933	AI458933	tk10a06.x
C 402	13	37.1	88	9	AA302701	475	12.8	36.6	84	10	R05954	R05954	Y689106.s1
C 403	13	37.1	88	10	N29378	C 476	12.8	36.6	85	12	A2485432	A2485432	1M0312P17
C 404	13	37.1	89	9	AI194799	C 477	12.8	36.6	86	9	AA253794	AA253794	mw03f07.r
C 405	13	37.1	90	9	AI654260	C 478	12.8	36.6	86	10	B036185	B036185	BJ036185
C 406	13	37.1	93	10	R39462	C 479	12.8	36.6	86	10	BM052185	BM052185	ic98b10.x
C 407	13	37.1	94	10	WB8037	C 480	12.8	36.6	86	12	A2763222	A2763222	1M0558P05
C 408	13	37.1	95	12	A2660255	C 481	12.8	36.6	86	12	CNS03T09	CNS03T09	Tetracodon
C 409	13	37.1	96	10	F34932	C 482	12.8	36.6	87	12	AF039786	AF039786	AF039786
C 410	13	37.1	96	12	A2485549	C 483	12.8	36.6	87	12	FR0018486	FR0018486	F. rubripes
C 411	13	37.1	97	9	AI663413	C 484	12.8	36.6	88	10	BM026911	BM026911	FL12b12.y
C 412	13	37.1	97	9	AA580891	C 485	12.8	36.6	88	12	A2784747	A2784747	2M0027B09
C 413	13	37.1	97	10	BJ034034	486	12.8	36.6	89	10	W12556	W12556	ma59e08.r1
C 414	13	37.1	97	12	A2513981	C 487	12.8	36.6	89	12	AZ403820	AZ403820	1M0171O24
C 415	13	37.1	97	12	B33978	C 488	12.8	36.6	91	9	AI126208	AI126208	qdb6f11.x
C 416	13	37.1	98	9	AF211614	C 489	12.8	36.6	91	9	AI931845	AI931845	u166904.x
C 417	13	37.1	98	9	AI973787	C 490	12.8	36.6	91	10	BE578422	BE578422	602092816
C 418	13	37.1	98	10	T25794	C 491	12.8	36.6	92	12	BH218633	BH218633	100608D1
C 419	13	37.1	98	12	BE718537	C 492	12.8	36.6	92	12	A2310944	A2310944	1M0026F12
C 420	13	37.1	98	12	CNS04PYV	C 493	12.8	36.6	93	12	A2992806	A2992806	2M0277P03
C 421	13	37.1	99	9	AI006438	C 494	12.8	36.6	94	9	AA444177	AA444177	AB320
C 422	13	37.1	99	10	BE718390	C 495	12.8	36.6	95	9	AA121929	AA121929	zm24f11.s
C 423	13	37.1	100	9	AA279164	C 496	12.8	36.6	95	9	AV914458	AV914458	AV914458
C 424	13	37.1	100	9	AAW38942	C 497	12.8	36.6	95	12	A2437964	A2437964	1M0225D17
C 425	13	37.1	100	9	AA428424	C 498	12.8	36.6	95	12	A2633214	A2633214	1M0486D13
C 426	13	37.1	100	10	BF877993	C 499	12.8	36.6	95	12	BH222731	BH222731	1006108H0
C 427	13	37.1	100	10	BM403549	C 500	12.8	36.6	96	9	AA270953	AA270953	xs06f12.x
C 428	13	37.1	100	10	W84967	C 501	12.8	36.6	96	10	BG792870	BG792870	UTSW_H5E6
C 429	13	37.1	100	12	BH612928	C 502	12.8	36.6	96	12	A2769904	A2769904	1M0571H02
C 430	12.8	36.6	21	12	AZ801236	C 503	12.8	36.6	97	9	AA897326	AA897326	a147e03.s
C 431	12.8	36.6	27	12	AZ997581	C 504	12.8	36.6	97	9	AI950903	AI950903	ws56g12.x
C 432	12.8	36.6	29	12	AG019559	C 505	12.8	36.6	97	9	AA198324	AA198324	pn1-b.pk0
C 433	12.8	36.6	35	12	TA386F0Q	C 506	12.8	36.6	97	9	AA617925	AA617925	ng02a06.s
C 434	12.8	36.6	37	9	AA906610	C 507	12.8	36.6	97	12	A2457629	A2457629	1M0279F12
C 435	12.8	36.6	37	9	AI302081	C 508	12.8	36.6	98	9	AA795589	AA795589	2M0255B01
C 436	12.8	36.6	37	12	A2760974	C 509	12.8	36.6	99	9	AI087352	AI087352	vg97e02.r
C 437	12.8	36.6	37	12	A2760974	C 510	12.8	36.6	99	9	AU009022	AU009022	o26e06.x
C 438	12.8	36.6	40	10	H30578	C 511	12.8	36.6	99	9	AU009026	AU009026	1M008072
C 439	12.8	36.6	41	10	BI196943	C 512	12.8	36.6	99	9	AU009026	AU009026	1M009026
C 440	12.8	36.6	48	12	A2777027	C 513	12.8	36.6	99	9	AA494151	AA494151	ng98d09.s
C 441	12.8	36.6	50	9	AU105320	C 514	12.8	36.6	99	10	BE901442	BE901442	1M0079N04
C 442	12.8	36.6	50	12	TA28AA04P	C 515	12.8	36.6	99	12	A2812711	A2812711	2M0079N04
C 443	12.8	36.6	52	12	AZ419921	C 516	12.8	36.6	99	12	BH224985	BH224985	1006122H1
C 444	12.8	36.6	52	12	BH625191	C 517	12.8	36.6	100	9	AA017565	AA017565	ze39h04.s
C 445	12.8	36.6	53	9	AI906692	C 518	12.8	36.6	100	9	AA896835	AA896835	RCO-NN05
C 446	12.8	36.6	55	9	AI736052	C 519	12.8	36.6	100	9	AA9598030	AA9598030	RCO-BN05
C 447	12.8	36.6	58	9	AI414138	C 520	12.8	36.6	100	9	AA454827	AA454827	z79c05.s
C 448	12.8	36.6	60	9	AA426872	C 521	12.8	36.6	100	10	BG277705	BG277705	ux60a10.y
C 449	12.8	36.6	60	10	C00950	C 522	12.8	36.6	100	10	BG330231	BG330231	f231-117
C 450	12.8	36.6	60	12	A2798400	C 523	12.8	36.6	100	10	BI497077	BI497077	d1131f06.
C 451	12.8	36.6	61	9	AA293064	C 524	12.8	36.6	100	10	BE667590	BE667590	7488c01.s
C 452	12.8	36.6	63	12	AZ422518	C 525	12.6	36.0	22	9	AA996014	AA996014	os26d08.s
C 453	12.8	36.6	64	9	AA717308	C 526	12.6	36.0	29	12	AZ929212	AZ929212	2M0276H15
C 454	12.8	36.6	65	9	AA614974	C 527	12.6	36.0	34	9	AI444328	AI444328	fb25f08.x
C 455	12.8	36.6	66	12	BH000352	C 528	12.6	36.0	37	12	BH000751	BH000751	2M0288L16

529	12.6	36.0	41	10	BI091365	BI091365 602859226	602	12.6	36.0	90	12	AZ443378	AZ443378 1M0238B05
530	12.6	36.0	47	12	BH624301	BH624301 1007105H0	603	12.6	36.0	90	12	BH226319	BH226319 1006131E0
531	12.6	36.0	48	10	BG390427	BG390427 602416059	604	12.6	36.0	91	10	AA125982	AA125982 zp27b04.r
532	12.6	36.0	49	9	AA433110	AA433110 v934903.r	605	12.6	36.0	91	10	BF248060	BF248060 601855209
533	12.6	36.0	50	9	AUI04138	AUI04138 AUI04138	606	12.6	36.0	91	10	BF467064	BF467064 UT-M-CG0P
534	12.6	36.0	50	9	AUI04282	AUI04282 AUI04282	607	12.6	36.0	91	12	AZ786320	AZ786320 2M0031E17
535	12.6	36.0	50	9	AUI05769	AUI05769 AUI05769	608	12.6	36.0	92	9	AA912724	AA912724 o141b03.s
536	12.6	36.0	50	9	AUI07240	AUI07240 AUI07240	609	12.6	36.0	92	10	H283289	H283289 y058h11.s1
537	12.6	36.0	50	9	AUI07242	AUI07242 AUI07242	610	12.6	36.0	92	12	AZ760407	AZ760407 1M0554H10
538	12.6	36.0	52	9	AA999971	AA999971 ov06c12.s	611	12.6	36.0	93	12	AA721402	AA721402 n274a03.s
539	12.6	36.0	54	12	AZ645918	AZ645918 1M0511L07	612	12.6	36.0	93	12	AZ333809	AZ333809 1M0157J02
540	12.6	36.0	54	12	AZ979086	AZ979086 2M0255107	613	12.6	36.0	93	12	AZ784753	AZ784753 2M0027G19
541	12.6	36.0	55	12	AQ025823	AQ025823 1(2)K0723	614	12.6	36.0	94	10	N55915	N55915 J4075F Huma
542	12.6	36.0	60	9	AA208720	AA208720 mub3e07.r	615	12.6	36.0	95	9	A1669223	A1669223 wc13d10.x
543	12.6	36.0	60	12	AZ834000	AZ834000 2M0116019	616	12.6	36.0	95	9	A1749417	A1749417 a123b03.x
544	12.6	36.0	61	9	A1190147	A1190147 qd57b01.x	617	12.6	36.0	95	12	AZ784382	AZ784382 2M0027C03
545	12.6	36.0	61	9	AA833601	AA833601 AV833601	618	12.6	36.0	95	12	BH632640	BH632640 1007096D0
546	12.6	36.0	61	9	AA581081	AA581081 nd13b07.s	619	12.6	36.0	96	12	AQ050455	AQ050455 nxb0004a
547	12.6	36.0	61	12	BH625998	BH625998 1007110F0	620	12.6	36.0	96	12	AZ441431	AZ441431 1M0233J08
548	12.6	36.0	62	12	BH410648	BH410648 1007019D0	621	12.6	36.0	97	9	AA777516	AA777516 z102g11.s
549	12.6	36.0	63	10	BM128209	BM128209 f110h07.y	622	12.6	36.0	97	9	AA430669	AA430669 zw26d03.s
550	12.6	36.0	64	9	AA170150	AA170150 ms81g12.r	623	12.6	36.0	97	10	BG143103	BG143103 1893e09.y
551	12.6	36.0	64	10	BE636314	BE636314 SMOVL2CAS	624	12.6	36.0	97	10	R46417	R46417 y152a07.r1
552	12.6	36.0	65	12	AZ373985	AZ373985 1M0126C04	625	12.6	36.0	97	12	AZ784030	AZ784030 2M0026M17
553	12.6	36.0	65	12	AZ377830	AZ377830 1M0132A22	626	12.6	36.0	97	12	CNS042N5	AL271706 Tetradon
554	12.6	36.0	68	10	BE845271	BE845271 AD09C06T7	627	12.6	36.0	98	12	AZ327962	AZ327962 1M0051F12
555	12.6	36.0	68	12	AZ620190	AZ620190 1M0452M14	628	12.6	36.0	98	9	A1434944	A1434944 t146e03.x
556	12.6	36.0	69	12	AZ434020	AZ434020 1M0220P08	629	12.6	36.0	99	12	AZ596257	AZ596257 1M0409I24
557	12.6	36.0	69	12	AZ632012	AZ632012 1M0486O21	630	12.6	36.0	99	12	AZ837397	AZ837397 2M013G11
558	12.6	36.0	69	12	TA205G10P	AL479149 T. bruce1	631	12.6	36.0	100	9	AA862553	AA862553 o144b08.s
559	12.6	36.0	70	9	AA790132	AA790132 v81d10.r	632	12.6	36.0	100	9	A1123109	A1123109 qe85c05.s
560	12.6	36.0	70	9	A1122990	A1122990 ok36a09.s	633	12.6	36.0	100	10	B1000502	B1000502 PMO-HN007
561	12.6	36.0	71	12	BH233453	BH233453 1006173G1	634	12.6	36.0	100	10	BM077292	BM077292 CIT000062
562	12.6	36.0	71	12	TA313E12P	AL465362 T. bruce1	635	12.6	36.0	100	10	BM077292	BM077292 CIT000062
563	12.6	36.0	71	12	TA307B01P	AL490546 T. bruce1	636	12.6	36.0	100	10	N85472	N85472 J3651F Huma
564	12.6	36.0	72	9	AA212693	AA212693 mw78d05.r	637	12.6	36.0	100	10	W15991	W15991 mb59c03.r1
565	12.6	36.0	72	9	AA2170378	AA2170378 xn60f01.x	638	12.6	36.0	100	10	BF725074	BF725074 bx11h08.y
566	12.6	36.0	73	9	A1718182	A1718182 as49g09.x	639	12.6	36.0	100	12	AZ410813	AZ410813 1M0183B23
567	12.6	36.0	73	9	A1940872	A1940872 sb79a02.y	640	12.6	36.0	100	12	AZ869672	AZ869672 2M0181E22
568	12.6	36.0	73	10	BF030695	BF030695 601560088	641	12.6	35.4	223	12	AZ954682	AZ954682 2M0220P23
569	12.6	36.0	74	10	N20347	N20347 yx38f05.s1	642	12.6	35.4	225	12	AZ621312	AZ621312 1M0434P19
570	12.6	36.0	74	12	AZ918333	AZ918333 1006004A1	643	12.6	35.4	229	12	AZ412411	AZ412411 1M0185A23
571	12.6	36.0	75	10	BF711709	BF711709 MI-P-E6-a	644	12.6	35.4	30	12	AZ793935	AZ793935 2M0047P22
572	12.6	36.0	76	9	AA884711	AA884711 am18f05.s	645	12.6	35.4	37	10	B7053200	B7053200 B0053200
573	12.6	36.0	76	9	A1117174	A1117174 v659f08.r	646	12.6	35.4	37	12	AZ848874	AZ848874 2M0150N02
574	12.6	36.0	77	10	F32093	F32093 HSPD24386.H	647	12.6	35.4	37	12	TA72B12P	AL457094 T. bruce1
575	12.6	36.0	78	12	AZ785504	AZ785504 2M0029J24	648	12.6	35.4	40	9	AL680540	AL680540 Cw62c08.x
576	12.6	36.0	79	10	BG703962	BG703962 602687060	649	12.6	35.4	40	12	AZ592185	AZ592185 1M0402H23
577	12.6	36.0	79	10	BI461875	BI461875 603204203	650	12.6	35.4	42	12	AZ417609	AZ417609 1M0193C21
578	12.6	36.0	79	12	CNS01J0C0	AL168057 Tetradon	651	12.6	35.4	42	12	AZ939796	AZ939796 2M0198M21
579	12.6	36.0	80	10	C01681	C01681 HUMS000869	652	12.6	35.4	44	9	AM063178	AM063178 TMO3142.KR
580	12.6	36.0	81	9	AA155686	AA155686 zo70c12.r	653	12.6	35.4	46	9	AA847140	AA847140 o048b04.s
581	12.6	36.0	81	12	AZ619241	AZ619241 1M0451B04	654	12.6	35.4	50	9	AUI03454	AUI03454 AUI03454
582	12.6	36.0	81	12	AZ762084	AZ762084 1M0556H18	655	12.6	35.4	50	9	AUI04845	AUI04845 AUI04845
583	12.6	36.0	82	9	AA080064	AA080064 mm34d03.r	656	12.6	35.4	51	10	R96023	R96023 y183a11.s1
584	12.6	36.0	82	9	A1491873	A1491873 t001g10.x	657	12.6	35.4	51	9	A1608507	A1608507 vc73h03.y
585	12.6	36.0	82	12	B42503	B42503 HS-1056-A1-	658	12.6	35.4	51	12	AZ314162	AZ314162 1M0030O14
586	12.6	36.0	83	9	A1424173	A1424173 t163a11.x	659	12.6	35.4	52	9	AA717460	AA717460 v193f08.r
587	12.6	36.0	83	12	AZ694084	AZ694084 AS1-ZH8BG	660	12.6	35.4	52	10	BU035097	BU035097 BU035097
588	12.6	36.0	84	10	BE350448	BE350448 hc92e09.x	661	12.6	35.4	55	9	AA661767	AA661767 nv04f06.s
589	12.6	36.0	84	12	AZ409131	AZ409131 1M0180O16	662	12.6	35.4	55	9	A1241482	A1241482 qb69c04.x
590	12.6	36.0	85	9	AA036504	AA036504 m159c08.r	663	12.6	35.4	55	9	A1658701	A1658701 tu22e09.r
591	12.6	36.0	85	9	AA937049	AA937049 o172f09.s	664	12.6	35.4	55	9	AA509624	AA509624 v919h09.r
592	12.6	36.0	85	9	AA629157	AA629157 af60f02.s	665	12.6	35.4	56	12	AZ424951	AZ424951 1M0204K15
593	12.6	36.0	85	10	BE1677348	BE1677348 1899h02.x	666	12.6	35.4	56	12	AZ962300	AZ962300 2M0263C06
594	12.6	36.0	85	10	BE913265	BE913265 601668266	667	12.6	35.4	56	12	TA116F01P	AL462530 T. bruce1
595	12.6	36.0	86	10	H55733	H55733 CHR220672.C	668	12.6	35.4	57	9	A1587809	A1587809 mpa2c06.y
596	12.6	36.0	88	10	W34393	W34393 mc58g03.r1	669	12.6	35.4	57	12	AZ843100	AZ843100 2M0141N14
597	12.6	36.0	88	12	BH217037	BH217037 1006051A0	670	12.6	35.4	58	9	AA068046	AA068046 mms59e05.r
598	12.6	36.0	89	9	AA883848	AA883848 am22g03.s	671	12.6	35.4	58	10	BG747162	BG747162 602704386
599	12.6	36.0	89	12	AZ308616	AZ308616 1M0011H18	672	12.6	35.4	58	10	D21022	D21022 HUMS02005
600	12.6	36.0	89	12	CNS02DV4	AL192937 Tetradon	673	12.6	35.4	59	12	AZ646147	AZ646147 1M0512K08
601	12.6	36.0	90	9	A1089487	A1089487 qb10a11.x	674	12.6	35.4	59	12	AZ799788	AZ799788 2M0057M20

C 675	12.4	35.4	59	12	BH218615	BH218615 1006080B1	748	12.4	35.4	93	9	AV860901	AV860901 AV860901
C 676	12.4	35.4	61	9	AA714673	AA714673 nx91F09.s	C 749	12.4	35.4	93	10	BI528914	BI528914 1024094E0
C 677	12.4	35.4	61	9	AA281867	AA281867 xt07C05.r	C 750	12.4	35.4	93	10	BI531215	BI531215 1024112B0
C 678	12.4	35.4	61	9	AA553640	AA553640 nk82d12.s	C 751	12.4	35.4	93	12	AZ440592	AZ440592 1M0231B15
C 679	12.4	35.4	62	9	AA081448	AA081448 zn06G04.r	C 752	12.4	35.4	93	12	AZ762170	AZ762170 1M0556H24
C 680	12.4	35.4	63	12	AA655452	AA655452 1M0530L17	C 753	12.4	35.4	94	9	AI801228	AI801228 t08G006.x
C 681	12.4	35.4	64	9	AI285583	AI285583 q08T06.x	C 754	12.4	35.4	94	9	AI886214	AI886214 wm08B01.x
C 682	12.4	35.4	64	9	AI937013	AI937013 wp72D01.x	C 755	12.4	35.4	94	9	AI966672	AI966672 sc54H06.y
C 683	12.4	35.4	64	10	BG938529	BG938529 cn26G02.x	C 756	12.4	35.4	94	10	H14298	H14298 ym63C01.r1
C 684	12.4	35.4	64	10	BE636351	BE636351 SMOVL2CAS	C 757	12.4	35.4	94	10	R18648	R18648 yf97e03.r1
C 685	12.4	35.4	68	9	AV922284	AV922284 AV922264	C 758	12.4	35.4	94	12	AZ760230	AZ760230 1M0553M15
C 686	12.4	35.4	69	10	BF308890	BF308890 601894529	C 759	12.4	35.4	95	9	AA291826	AA291826 zt28E01.r
C 687	12.4	35.4	70	12	BH217857	BH217857 1006060E0	C 760	12.4	35.4	95	9	AM693206	AM693206 NF063C06S
C 688	12.4	35.4	72	9	AA527338	AA527338 ng36G06.s	C 761	12.4	35.4	95	10	F34318	F34318 HSPD29103.H
C 689	12.4	35.4	72	10	CO1050	CO1050 HUMGS000716	C 762	12.4	35.4	95	10	T95120	T95120 ye44f06.s1
C 690	12.4	35.4	73	10	AA854348	AA854348 aj73F03.s	C 763	12.4	35.4	95	12	AZ360003	AZ360003 1M0103A22
C 691	12.4	35.4	73	10	TI1467	TI1467 CHR90033 Ch	C 764	12.4	35.4	96	10	BI262024	BI262024 602953423
C 692	12.4	35.4	73	10	BEA20493	BEA20493 SMOVL2CAS	C 765	12.4	35.4	96	10	R94761	R94761 yf71f08.s1
C 693	12.4	35.4	73	12	AA405623	AA405623 1M0174103	C 766	12.4	35.4	96	12	AZ366275	AZ366275 1M0115L18
C 694	12.4	35.4	75	10	BF465862	BF465862 UI-M-CGDP	C 767	12.4	35.4	96	12	AZ474130	AZ474130 1M0290J20
C 695	12.4	35.4	75	12	AA585289	AA585289 1M0390E23	C 768	12.4	35.4	96	12	AZ774363	AZ774363 2M0003F11
C 696	12.4	35.4	76	9	AA618253	AA618253 ng16G09.s	C 769	12.4	35.4	96	12	BTAA16740	BTAA16740
C 697	12.4	35.4	76	12	N23106	N23106 yw43h07.s1	C 770	12.4	35.4	97	9	AA853669	AA853669 NHTBCae07
C 698	12.4	35.4	76	12	BH409808	BH409808 1007014E0	C 771	12.4	35.4	97	9	AA880530	AA880530 wp91s12.r
C 699	12.4	35.4	77	9	AAW01978	AAW01978 sg81e03.y	C 772	12.4	35.4	97	9	AA105625	AA105625 tmh6C06.r
C 700	12.4	35.4	77	9	AA566996	AA566996 1050 L0b1	C 773	12.4	35.4	97	9	AU009025	AU009025 AU009025
C 701	12.4	35.4	77	12	AA620057	AA620057 1M0452B10	C 774	12.4	35.4	97	12	AZ331617	AZ331617 1M0059J10
C 702	12.4	35.4	78	9	AI904218	AI904218 PM-BR046-	C 775	12.4	35.4	97	12	AA611344	AA611344 1M0437F07
C 703	12.4	35.4	78	9	AA458049	AA458049 vf76d12.r	C 776	12.4	35.4	98	9	AA746000	AA746000 ny94B07.s
C 704	12.4	35.4	79	9	AA128193	AA128193 z192d12.r	C 777	12.4	35.4	98	9	AI269321	AI269321 q169B08.x
C 705	12.4	35.4	79	9	AI921370	AI921370 wo24G04.x	C 778	12.4	35.4	98	9	AM638196	AM638196 bl67C03.w
C 706	12.4	35.4	79	9	AA287452	AA287452 z552h11.s	C 779	12.4	35.4	98	9	AI569199	AI569199 tR3h03.x
C 707	12.4	35.4	79	9	AA553197	AA553197 v113f11.r	C 780	12.4	35.4	99	10	BF990091	BF990091 MR3-GN014
C 708	12.4	35.4	79	10	BA082016	BA082016 BJ082016	C 781	12.4	35.4	99	10	BC405954	BC405954 sac4-GB055
C 709	12.4	35.4	80	10	N25010	N25010 vx17f10.r1	C 782	12.4	35.4	99	12	BF033738	BF033738 BU033738
C 710	12.4	35.4	80	10	BJ076385	BJ076385 v144G02.r	C 783	12.4	35.4	99	12	AF149604	AF149604 AF149604
C 711	12.4	35.4	82	9	AA845785	AA845785 BJ076385	C 784	12.4	35.4	99	12	AA355543	AA355543 1M0095G07
C 712	12.4	35.4	82	9	AA962612	AA962612 ak77h10.s	C 785	12.4	35.4	100	9	AA885029	AA885029 am41e03.s
C 713	12.4	35.4	82	10	BG222618	AA962612 or35h11.s	C 786	12.4	35.4	100	9	AA937861	AA937861 nw90B10.s
C 714	12.4	35.4	82	10	H28417	H28417 yo53h01.s1	C 787	12.4	35.4	100	9	AJ395728	AJ395728 AJ395728
C 715	12.4	35.4	82	12	AZ794700	AZ794700 2M0048P03	C 788	12.4	35.4	100	9	AM431886	AM431886 73277 MAR
C 716	12.4	35.4	83	9	AA530673	AA530673 v144G02.r	C 789	12.4	35.4	100	9	AM577291	AM577291 RC5-BT050
C 717	12.4	35.4	83	10	BT4993486	BT4993486 df101B09.	C 790	12.4	35.4	100	9	AM860735	AM860735 OVO-CT038
C 718	12.4	35.4	84	9	AI332551	AI332551 qp82B09.x	C 791	12.4	35.4	100	9	BE071154	BE071154 RC3-BT050
C 719	12.4	35.4	84	10	BG935148	BG935148 SL1-0457	C 792	12.4	35.4	100	9	BE151755	BE151755 OVO-HT010
C 720	12.4	35.4	84	12	AZ782133	AZ782133 2M0022D10	C 793	12.4	35.4	100	10	BF875679	BF875679 QV3-ET010
C 721	12.4	35.4	85	9	AA255902	AA255902 z529C06.s	C 794	12.4	35.4	100	10	BF961658	BF961658 QV2-NN004
C 722	12.4	35.4	85	12	AZ918770	AZ918770 1006007B0	C 795	12.4	35.4	100	10	BR376323	BR376323 601228693
C 723	12.4	35.4	85	12	BH227184	BH227184 1006137H0	C 796	12.4	35.4	100	10	BE400130	BE400130 AMB011.F0
C 724	12.4	35.4	86	9	BE217335	BE217335 459/669-T	C 797	12.4	35.4	100	10	BE400130	BE400130 AMB011.F0
C 725	12.4	35.4	86	10	BG974863	BG974863 602842747	C 798	12.4	35.4	100	12	AZ829723	AZ829723 2M0107122
C 726	12.4	35.4	86	10	BF145981	BF145981 uy80d06.y	C 799	12.4	35.4	100	12	AZ770021	AZ770021 1M0571J16
C 727	12.4	35.4	86	12	BH229406	BH229406 1006152A1	C 800	12.4	35.4	100	12	AZ957207	AZ957207 2M0224E04
C 728	12.4	35.4	87	9	AI858457	AI858457 w138f02.x	C 801	12.4	35.4	100	12	AZ786137	AZ786137 1M0031E01
C 729	12.4	35.4	87	10	BI838602	BI838602 603086284	C 802	12.4	35.4	100	12	AA663451	AA663451 1M0543P06
C 730	12.4	35.4	87	12	AZ809937	AZ809937 2M0074L07	C 803	12.4	35.4	100	9	AI421552	AI421552 t126d07.x
C 731	12.4	35.4	88	9	AI564643	AI564643 tq78B06.x	C 804	12.4	35.4	100	9	AA810394	AA810394 nx75H04.s
C 732	12.4	35.4	88	9	AU014246	AU014246 AU014246	C 805	12.4	35.4	100	9	AI434159	AI434159 tH40B11.x
C 733	12.4	35.4	88	9	AU014247	AU014247 AU014247	C 806	12.4	35.4	100	9	AA687683	AA687683 nv11f09.s
C 734	12.4	35.4	88	9	AA614999	AA614999 vc03h04.r	C 807	12.4	35.4	100	9	BM939737	BM939737 50072-2-1
C 735	12.4	35.4	88	10	N83307	N83307 EC0050F Hum	C 808	12.4	35.4	100	9	C20880	C20880 HUMGS00494
C 736	12.4	35.4	88	12	BH226539	BH226539 1006132G1	C 809	12.4	35.4	100	9	AI023230	AI023230 ov78d11.s
C 737	12.4	35.4	89	9	AI1748392	AI1748392 sb52B11.y	C 810	12.4	35.4	100	12	AZ590749	AZ590749 1M0400004
C 738	12.4	35.4	89	9	AI938738	AI938738 sb58C07.y	C 811	12.4	35.4	100	9	AU104658	AU104658 AU104658
C 739	12.4	35.4	89	9	AJ399326	AJ399326 AJ399326	C 812	12.4	35.4	100	9	AU104694	AU104694 AU104694
C 740	12.4	35.4	89	10	BG486633	BG486633 gd02h11.x	C 813	12.4	35.4	100	9	AU105765	AU105765 AU105765
C 741	12.4	35.4	89	10	BM008683	BM008683 603618359	C 814	12.4	35.4	100	9	AU106986	AU106986 AU106986
C 742	12.4	35.4	90	9	AA711952	AA711952 vu29a12.r	C 815	12.4	35.4	100	9	AU107239	AU107239 AU107239
C 743	12.4	35.4	90	9	BE043294	BE043294 hK49F04.y	C 816	12.4	35.4	100	9	AU107363	AU107363 AU107363
C 744	12.4	35.4	92	9	AJ271464	AJ271464 AJ271464	C 817	12.4	35.4	100	9	AU107462	AU107462 AU107462
C 745	12.4	35.4	92	12	AZ791488	AZ791488 2M0041L19	C 818	12.4	35.4	100	12	AZ785616	AZ785616 2M0029J09
C 746	12.4	35.4	92	12	AZ791488	AZ791488 2M0041L19	C 819	12.4	35.4	100	12	B02595	B02595 cSRL-156G5-S
C 747	12.4	35.4	93	9	AI664027	AI664027 ue76D09.r	C 820	12.4	35.4	100	9	AA861532	AA861532 ak17g10.s

C 821	12.2	34.9	52	9	A1920194	1724 Pine	C 894	12.2	34.9	82	9	AA610720	AA610720 np92c06.s
C 822	12.2	34.9	52	12	A2957010	A2957010 2M0223B18	C 895	12.2	34.9	82	10	BF633575	BF633575 NF057H04D
C 823	12.2	34.9	54	12	A2612626	A2612626 1M0439C06	C 896	12.2	34.9	82	12	A2795408	A2795408 2M0049E07
C 824	12.2	34.9	55	9	AA553930	AA553930 nk34d11.s	C 897	12.2	34.9	82	12	BH614963	BH614963 K02316-5
C 825	12.2	34.9	56	9	AV833096	AV833096 AV833096	C 898	12.2	34.9	83	9	AA064479	AA064479 m150a04.r
C 826	12.2	34.9	56	10	BJ078630	BJ078630 BJ078630	C 899	12.2	34.9	83	9	AA688244	AA688244 nv17e07.s
C 827	12.2	34.9	57	12	A2920666	A2920666 1006021A0	C 900	12.2	34.9	83	9	AA897350	AA897350 a147h08.s
C 828	12.2	34.9	57	12	AA889441	AA889441 a181h04.s	C 901	12.2	34.9	83	9	AA910028	AA910028 ur88b06.x
C 829	12.2	34.9	57	9	BE059158	BE059158 1007019D1	C 902	12.2	34.9	83	12	A2851870	A2851870 2M0154M13
C 830	12.2	34.9	57	12	BH410651	BH410651 1007019D1	C 903	12.2	34.9	84	9	AA004678	AA004678 ws90a10.x
C 831	12.2	34.9	58	9	AA832068	AA832068 oc94e12.s	C 904	12.2	34.9	85	9	AA884781	AA884781 em20d08.s
C 832	12.2	34.9	58	9	A1355421	A1355421 qt77e07.x	C 905	12.2	34.9	85	9	A1545968	A1545968 fb6e08.y
C 833	12.2	34.9	58	12	BH411667	BH411667 1007023E0	C 906	12.2	34.9	85	9	A1763114	A1763114 w106c07.x
C 834	12.2	34.9	60	10	H85975	H85975 yf02904.s1	C 907	12.2	34.9	85	9	A1965018	A1965018 fc85g06.y
C 835	12.2	34.9	60	10	BE615206	BE615206 601281178	C 908	12.2	34.9	85	9	A1967903	A1967903 lJlrnpst
C 836	12.2	34.9	60	12	CNS0403X	AL268423 Tetradon	C 909	12.2	34.9	85	9	AA253613	AA253613 mw95a12.r
C 837	12.2	34.9	61	9	AA019856	AA019856 zee60b02.s	C 910	12.2	34.9	85	10	R81027	R81027 y194h07.r1
C 838	12.2	34.9	61	9	A1973695	A1973695 sdo8e09.y	C 911	12.2	34.9	85	10	BF062644	BF062644 7h63c01.x
C 839	12.2	34.9	61	9	AA250403	AA250403 mw16e11.r	C 912	12.2	34.9	86	9	AA937258	AA937258 nz54b07.s
C 840	12.2	34.9	62	9	A1253516	A1253516 ag33e04.x	C 913	12.2	34.9	86	9	A1420838	A1420838
C 841	12.2	34.9	63	10	BF026783	BF026783 601672053	C 914	12.2	34.9	86	10	H39321	H39321
C 842	12.2	34.9	63	12	A2465840	A2465840 1M0276102	C 915	12.2	34.9	86	12	A2352672	A2352672
C 843	12.2	34.9	64	9	A1306392	A1306392 qn12f09.x	C 916	12.2	34.9	86	12	A2784704	A2784704
C 844	12.2	34.9	64	9	AA409554	AA409554 SMOV3MCAM	C 917	12.2	34.9	87	9	AA702456	AA702456
C 845	12.2	34.9	64	9	AA626483	AA626483 SMOVAFCAP	C 918	12.2	34.9	87	9	AA302971	AA302971
C 846	12.2	34.9	64	9	AA449247	AA449247 zX04C10.s	C 919	12.2	34.9	87	9	AA467643	AA467643
C 847	12.2	34.9	64	9	AA510349	AA510349 vq36a09.r	C 920	12.2	34.9	87	12	A2831735	A2831735
C 848	12.2	34.9	65	10	R97968	R97968 yq74f11.s1	C 921	12.2	34.9	88	9	AA908420	AA908420 og78b09.s
C 849	12.2	34.9	67	10	AA576590	AA576590 nm66g08.s	C 922	12.2	34.9	88	9	AA558306	AA558306 l135a10.s
C 850	12.2	34.9	67	10	BM124842	BM124842 L0546A03-	C 923	12.2	34.9	88	10	BM055186	BM055186 l691e11.y
C 851	12.2	34.9	67	12	A2822974	A2822974 2M0096N10	C 924	12.2	34.9	88	12	CNS01Y21	AA117655 Tetradon
C 852	12.2	34.9	68	9	AA911279	AA911279 oe75c11.s	C 925	12.2	34.9	89	9	AA212943	AA212943
C 853	12.2	34.9	68	9	A1313605	A1313605 nfc3e04.x	C 926	12.2	34.9	89	10	B1219289	B1219289
C 854	12.2	34.9	68	9	AA534601	AA534601 nfc1c05.x	C 927	12.2	34.9	89	10	R28931	R28931
C 855	12.2	34.9	69	9	AA173429	AA173429 xj06e10.x	C 928	12.2	34.9	90	9	AA929860	AA929860 vss5e01.r
C 856	12.2	34.9	70	9	AA647668	AA647668 vp03d02.r	C 929	12.2	34.9	90	10	B1520634	B1520634 603071591
C 857	12.2	34.9	70	9	AA855652	AA855652 vw70g01.r	C 930	12.2	34.9	90	12	A2464625	A2464625 1M0274003
C 858	12.2	34.9	71	9	AA962824	AA962824 oo93c12.s	C 931	12.2	34.9	90	12	A2624148	A2624148 1M0462004
C 859	12.2	34.9	71	9	BE226233	BE226233 lal7e09.y	C 932	12.2	34.9	90	12	FR0014755	AL005944 F.rubrtpe
C 860	12.2	34.9	72	10	BM434757	BM434757 lrr13c11	C 933	12.2	34.9	91	9	AA059539	AA059539 m163a08.r
C 861	12.2	34.9	72	12	AF219044	AF219044 AF219044	C 934	12.2	34.9	91	9	A1342887	A1342887 qo32b07.x
C 862	12.2	34.9	72	12	CNS03370	AL225791 Tetradon	C 935	12.2	34.9	91	9	A1810035	A1810035 wt79d01.x
C 863	12.2	34.9	73	9	AA727692	AA727692 vv02e07.r	C 936	12.2	34.9	91	9	AU007424	AU007424 AA007424
C 864	12.2	34.9	73	9	A1785511	A1785511 u143d02.x	C 937	12.2	34.9	91	9	AA415962	AA415962 vf38f05.r
C 865	12.2	34.9	73	9	AA403128	AA403128 zw66h11.s	C 938	12.2	34.9	91	9	AA531137	AA531137 n51a00.s
C 866	12.2	34.9	73	9	AA434437	AA434437 zw25b08.s	C 939	12.2	34.9	91	10	BC234233	BC234233 dda38f06.
C 867	12.2	34.9	74	9	A1415804	A1415804 fb30c04.y	C 940	12.2	34.9	91	10	RS4725	RS4725 yj78h10.s1
C 868	12.2	34.9	74	12	A2877471	A2877471 2M0192K24	C 941	12.2	34.9	91	10	W14397	W14397 ma60a05.r1
C 869	12.2	34.9	75	12	A2589508	A2589508 1M0396J01	C 942	12.2	34.9	91	10	W36554	W36554 mb66f03.r1
C 870	12.2	34.9	76	9	AA035248	AA035248 zk24g04.s	C 943	12.2	34.9	91	10	W89986	W89986 m162e01.r1
C 871	12.2	34.9	76	9	AA144195	AA144195 mr75c02.r	C 944	12.2	34.9	91	12	A2638129	A2638129 1M0497D21
C 872	12.2	34.9	76	9	A1431367	A1431367 0005 C8tf	C 945	12.2	34.9	92	9	A1671958	A1671958 wc31e07.x
C 873	12.2	34.9	76	9	AL644798	AL644798 AL644798	C 946	12.2	34.9	92	9	A1961905	A1961905 wt40f06.x
C 874	12.2	34.9	76	12	A2803101	A2803101 2M0063L13	C 947	12.2	34.9	92	12	TA181A03P	AL474307 T. bruce1
C 875	12.2	34.9	76	12	CNS02D10	AA1193491 Tetradon	C 948	12.2	34.9	93	9	AA1087500	AA1087500 SWMAC17
C 876	12.2	34.9	77	9	AA755037	AA755037 vv79e06.r	C 949	12.2	34.9	93	9	AA159444	AA159444 zOT78C02.r
C 877	12.2	34.9	77	9	A1252082	A1252082 qv58b09.x	C 950	12.2	34.9	93	9	AA213329	AA213329 uo88c02.x
C 878	12.2	34.9	77	10	BM261553	BM261553 dda46a02.	C 951	12.2	34.9	93	9	AA458687	AA458687 aab6h01.r
C 879	12.2	34.9	78	9	AV932113	AV932113 AV932113	C 952	12.2	34.9	93	10	W35927	W35927 mc32a07.r1
C 880	12.2	34.9	78	10	BJ044592	BJ044592 BJ044592	C 953	12.2	34.9	93	10	Z19913	Z19913 H5AAA2YWS
C 881	12.2	34.9	79	9	AA973332	AA973332 op19g09.s	C 954	12.2	34.9	94	9	AA033711	AA033711 zk20d07.s
C 882	12.2	34.9	79	10	BM285360	BM285360 EST00010	C 955	12.2	34.9	94	9	AA052227	AA052227 mb47g10.r
C 883	12.2	34.9	79	10	BM493227	BM493227 EST00010	C 956	12.2	34.9	94	9	AA680654	AA680654 lmpfAm011
C 884	12.2	34.9	79	12	B01126	B01126 CSR1-126c1-	C 957	12.2	34.9	94	9	AA703885	AA703885 ag79b01.r
C 885	12.2	34.9	80	9	AA584913	AA584913 nm3c01.s	C 958	12.2	34.9	94	9	AA905937	AA905937 oJ83b03.s
C 886	12.2	34.9	80	10	B1175431	B1175431 OSTR044H3	C 959	12.2	34.9	94	9	AA165347	AA165347 zOB0h03.s
C 887	12.2	34.9	80	10	B1496497	B1496497 dfl125g04.	C 960	12.2	34.9	94	10	BE221289	BE221289 ht55c01.x
C 888	12.2	34.9	80	10	T82935	T82935 yd39g06.r1	C 961	12.2	34.9	94	10	W77301	W77301 me65e08.r1
C 889	12.2	34.9	80	12	A2566874	A2566874 227PvE07	C 962	12.2	34.9	94	12	A2623864	A2623864 1M0462D01
C 890	12.2	34.9	80	12	BH216830	BH216830 1006046H0	C 963	12.2	34.9	94	12	CNS03HRE	AL224643 Tetradon
C 891	12.2	34.9	80	12	CNS04MR	AL291792 Tetradon	C 964	12.2	34.9	95	9	AA064462	AA064462 m148f10.r
C 892	12.2	34.9	81	10	BG562156	BG562156 EREStee09	C 965	12.2	34.9	95	10	BE845229	BE845229 AD08C01T7
C 893	12.2	34.9	81	12	A2762211	A2762211 1M0556P20	C 966	12.2	34.9	95	12	TA240A04P	AL481566 T. bruce1

```

967 12.2 34.9 96 9 AJ282942 4A3A-P2B1
968 12.2 34.9 96 9 AM301631 Xr98h05.x
969 12.2 34.9 96 9 AM355279 PCOLC.PK0
970 12.2 34.9 96 10 T49495
971 12.2 34.9 96 10 BE977536
972 12.2 34.9 96 12 BH418324
973 12.2 34.9 97 10 BH784495
974 12.2 34.9 97 12 BH782064
975 12.2 34.9 97 12 BH234246
976 12.2 34.9 98 9 A1657116
977 12.2 34.9 98 9 A1720612
978 12.2 34.9 98 12 A2427428
979 12.2 34.9 98 12 A2804219
980 12.2 34.9 98 12 A2923038
981 12.2 34.9 99 9 AA064484
982 12.2 34.9 99 9 AA738943
983 12.2 34.9 99 10 T83784
984 12.2 34.9 99 12 A2342558
985 12.2 34.9 99 12 A2588377
986 12.2 34.9 100 9 A1292201
987 12.2 34.9 100 9 AM881486
988 12.2 34.9 100 9 BE041736
989 12.2 34.9 100 9 BE179164
990 12.2 34.9 100 9 AA619127
991 12.2 34.9 100 10 BF745311
992 12.2 34.9 100 10 BF170724
993 12.2 34.9 100 12 A2819462
994 12.2 34.3 23 12 A2374746
995 12.2 34.3 32 12 A2471070
996 12.2 34.3 34 9 A1539355
997 12.2 34.3 34 9 A1664262
998 12.2 34.3 35 12 A0254832
999 12.2 34.3 40 12 A2623260
1000 12.2 34.3 42 10 C58084 C58084 Yuj1

```

ALIGNMENTS

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RESULT 1
AZ773847 38 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0001009R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
LOCUS AZ773847
ACCESSION AZ773847
VERSION 1
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

```

```

REFERENCE 1 (bases 1 to 38)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
and Wright,D., Weiss,R., Stokes,R., Tinney,A., von Niederhausen,A.
M., Rose,M., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
and Wright,D., Weiss,R., Stokes,R., Tinney,A., von Niederhausen,A.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0001 row: F column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers

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FEATURES

source

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1. 38
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0001F09"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g147321419b1AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 12 a 6 c 10 g 10 t
ORIGIN
Query Match 53.1%; Score 18.6; DB 12; Length 38;
Best Local Similarity 84.0%; Pred. No. 3.4e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 catgtctagaatgggagatggatc 25
Db 14 CATGCTAGGATGGGATGCTAACA 38

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RESULT 2
AA668503 79 bp mRNA linear EST 20-NOV-1997
LOCUS ab86h11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone
DEFINITION IMAGE:853893 3' similar to TR:G1336628 G1336628 EGF REPEAT
TRANSMEMBRANE PROTEIN. ;, mRNA sequence.
ACCESSION AA668503
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE 1 (bases 1 to 79)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,C., Jost,S.,
Krizman,D., Kucada,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Stepcoe,M., Tan,F., Theisling,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

```

FEATURES

	source	1. .79 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:853893" /clone_lib="Stratagene fetal retina 937202" /sex="mixed" /lab_host="SOLR (kanamycin resistant)" /note="Vector: plusscript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt, pooled retinal tissue. Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGACGAG 3' -3' adaptor sequence: 5' CTCGACTTTT TTTT TTTT TTTT 3'"
BASE COUNT	29 a 19 c 17 g 14 t	
ORIGIN		
Query Match	49.7%; Score 17.4; DB 9; Length 79;	
Best Local Similarity	68.6%; Pred. No. 1.le+04;	
Matches	24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;	
Db	50 CTTGTCTGAATGGTGTTGTCTGCAGTCTCGACGT 16	
1 catgtctagaattggatggtgcaccttgacct 35		
RESULT 3		
AA954823/c	79 bp mRNA linear EST 07-JUL-1998	
LOCUS	AA954823	
DEFINITION	oc099d08..1 NCI-CGAP Kid6 Homo sapiens CDNA clone IMAGE:1574319 3'	
DESCRIPTION	similar to TR:061204 061204 EGF REPEAT TRANSMEMBRANE PROTEIN.	
ACCESSION	AA954823	
VERSION	AA954823.1 GI:3118518	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 79) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)	
JOURNAL COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@remail.nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmerit-Buck, M.D., Ph.D. CDNA Library Preparation: Stratagene, Inc. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLB at: www-bio.llnl.gov/dbirp/image/image.html Insert length: 549 Std Error: 0.00 Seq primer: -40ml3 fwd. RT from Amersham High quality sequence stop: 1.	
FEATURES		
Source	Location/Qualifiers	
	1. .79	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:1574319"	
	/clone_lib="NCI-CGAP_Kid6"	
	/sex="mixed"	
	/tissue_type="kidney tumor"	
	/lab_host="SOLR (kanamycin resistant)"	
	/note="Organ: kidney; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt, Pooled kidney tumors. 5' adaptor sequence: 5' GAATTCGGACGAG 3' 3' adaptor sequence: 5' CTCGACTTTT TTTT TTTT TTTT 3'"	
	CTCAGTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."	
BASE COUNT	26 a 19 c 16 g 15 t	
ORIGIN		

[illegible]

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VERSION      AI085281.1  GI:3423704
KEYWORDS
SOURCE
ORGANISM     human.
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    NC1/NINDS-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
AUTHORS      1 (bases 1 to 79)
              National Cancer Institute / National Institute of Neurological
              Disorders and Stroke, Brain Tumor Genome Anatomy Project
              (CGAP/BTGAAP), Tumor Gene Index
              Unpublished (1998)
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
              Ph.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
              Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NC1-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html

FEATURES
  source
    Trace considered overall poor quality
    Seq primer: -40m13 fwd. ET from Amersham
    High quality sequence stop: 1.
    Location/Qualifiers
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        /db_xref="taxon:9606"
        /clone="IMAGE:1750402"
        /clone_1lb="NC1-CGAP_Brn25"
        /tissue_type="anaplastic oligodendroglioma"
        /lab_host="IDH108"
        /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
        modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
        strand cDNA was primed with a Not I - oligo(dT) primer [5'/
        TGTACCAATCTGAGGTGGAGCGCGCCGCAATGAGGTGTTTGTGTTTTTTTTTTTTTTT
        T 3']; double-stranded cDNA was ligated to Eco RI
        adaptors (Pharmacia), digested with Not I and cloned into
        the Not I and Eco RI sites of the modified pT73 vector.
        Library is normalized, and was constructed by Bento
        Soares and M.Fatima Bonaldo."
BASE COUNT   30 a 17 c 16 g 16 t
ORIGIN
  Query Match      49.7%; Score 17.4; DB 9; Length 79;
  Best Local Similarity 68.6%; Pred. No. 1.1e+04;
  Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
  QY      1 catgctagaatggagatcgggctcactcggagcct 35
          | | | | | | | | | | | | | | | | | | |
          | | | | | | | | | | | | | | | | | | |
  Db      50 CTGTCTCGAATGGCTTTGTTCTCACTCGCACT 16

RESULT      6
LOCUS       AA142830
DEFINITION  79 bp mRNA linear EST 04-DEC-1996
IMAGE       504361 3' similar to TR:G1336628 GI336628 Esf REPEAT
TRANSMEMBRANE PROTEIN.; mRNA sequence.
ACCESSION   AA142830
VERSION     AA142830.1  GI:1712235
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 79)
            Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
            'M., Hultman, M., Kucaba, T., De, M., Lennon, G., Maitra, M., Parsons, J.,

```

TITLE	JOURNAL	COMMENT
Rickin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.	Unpublished (1995)	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
FEATURES	SOURCE	
1. 79		
/organism="Homo sapiens"		
/db_xref="GDB:3809349"		
/db_xref="taxon:9606"		
/clone="IMAGE:504361"		
/clone_lib="Soares_pregnant_uterus_NbHPV"		
/sex="female"		
/dev_stage="adult"		
/lab_host="DH10B"		
/note="Organ: uterus; Vector: pT73-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACGGAAGAAATTCGCGCGCCCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."		
BASE COUNT	29 a 19 c 17 g 14 t	
ORIGIN		
Query Match	49.7%; Score 17.4; DB 9; Length 79;	
Best Local Similarity	68.6%; Pred. No. 1.1e+04;	
Matches	24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;	
Oy	1 catgctagaatgggagtgagtcaccttgacct 35	
Db	50 CTTGTTCTGAATGGTGTGCTCAGTCTCGACGT 16	
RESULT 7		
LOCUS	AI675555 79 bp mRNA linear EST 17-DEC-1999	
DEFINITION	wc01h12.x1 NCI-CGAP Pr28 Homo sapiens cDNA clone IMAGE:2313959 3'	
ACCESSION	AI675555	
VERSION	AI675555.1 GI:4876035	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 79)	
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
COMMENT	Unpublished (1997)	
	Contact: Robert Strausberg, Ph.D.	
	Email: cgaps-rt@mail.nih.gov	
	Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.	
	CDNA Library Preparation: M. Bento Soares, Ph.D.	
	CDNA Library Arrayed by: Greg Lennon, Ph.D.	
	DNA Sequencing by: Washington University Genome Sequencing Center	
	clone distribution: NCI-CGAP clone distribution information can be	

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL:
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL0&tl=IL0-HT0156-
 251099-132-a03&tl=1999-10-25&tl=1)
 Seq primer: puc 18 forward
 High quality sequence start: 38
 High quality sequence stop: 100.
 Location/Qualifiers
 1..100
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="HT0156"
 /dev_stage="Adult"
 /note="Organ: head/neck; Vector: puc18; Site:1: SmaI;
 Site:2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 20 a 22 c 30 g 28 t
 ORIGIN

Query Match 46.9%; Score 16.4; DB 9; Length 100;
 Best Local Similarity 76.9%; Pred. NO. 2.6e+04;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 5 tctagaatgggagtgggctacctg 30
 || |||| | |||| |||| | ||
 Db 41 TCAGAGGAGGATGTGTCATGTG 66

RESULT 13 79 bp mRNA linear EST 29-DEC-1998
 AA723716/c
 LOCUS
 DEFINITION
 AB85f03.s1 Soares_NFL.T GBC_S1 Homo sapiens cDNA clone
 IMAGE:1325885.3' similar to TR:008567 008567 GUG-DOMAIN PROTEIN
 HOMER,, mRNA sequence.

ACCESSION AA723716 GI:2741423
 VERSION AA723716
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 79)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL COMMENT
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rt@mail.nih.gov

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Possible reversed clone: polyT not found
 Insert Length: 482 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 SOURCE
 1..79
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1325885"

/clone_id="Soares_NFL.T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: p7n3D-Pac (Pharmacia) with
 a modified polylinker; Site:1: Not I; Site:2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL9W, testis NHF, and B-cell
 NCI-CGAP-GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo.
 BASE COUNT 20 a 28 c 20 g 11 t
 ORIGIN

Query Match 46.3%; Score 16.2; DB 9; Length 79;
 Best Local Similarity 85.7%; Pred. NO. 3e+04;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 12 tggggatggggtacctctgga 32
 ||| | |||| |||| | ||||
 Db 50 TGGCTGTGGGCTCATCTCGA 30

RESULT 14 81 bp mRNA linear EST 12-FEB-1997
 AA166006/c
 LOCUS
 DEFINITION
 ms24d02.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:607875.5' similar to gb:U09189 Mus musculus lorixin gene,
 complete cds (MOUSE);, mRNA sequence.

ACCESSION AA166006 GI:1744553
 VERSION AA166006.1 GI:1744553
 KEYWORDS EST.

SOURCE house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 81)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisell,S., Kucab,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL COMMENT
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project

WASHU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:373307
 Seq primer: -28ml3 rev1 ET from Amersham.
 Location/Qualifiers

FEATURES
 SOURCE

1..81
 /organism="Mus musculus"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:607875"
 /clone_id="Stratagene mouse skin (#937313)"
 /sex="females"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: skin; Vector: pBluescript SK-; Site:1: EcoRI
 ; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo
 dt. Whole skin from 11 week old C57BL/6 female mice.

BASE COUNT 25 a 20 c 12 g 24 t

ORIGIN

Query Match 46.3%; Score 16.2; DB 9; Length 81;
 Best Local Similarity 72.4%; Pred. No. 3e+04;
 Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 ctgaatgggagatgggtactctgacc 34
 ||||||| ||| | ||||| ||| |

Db 57 CTGAAATGGAGGTAGTCATTCAGAAAC 29

RESULT 15

AA960093 58 bp mRNA linear EST 08-MAY-1998
 LOCUS ub54a10.s1 Soares-mammary-gland_NMLMG Mus musculus cDNA clone
 DEFINITION IMAGE:1381530 3' similar to TR:P70441 P70441 PROTEIN CO-FACTOR. ; ,
 mRNA sequence.

ACCESSION AA960093
 VERSION AA960093.1 GI:3125993
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 58)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubugue,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:903998

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Possible reversed clone: polyT not found
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES
 source 1.58
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:1381530"
 /clone_1lb="Soares.mammary-gland_NMLMG"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /tissue="mammary gland"
 /lab_host="DH10B"
 /note="Vector: p77T3D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from mammary
 gland tissue from a lactating female, and was then primed
 with a Not I - oligo(dT) primer. Double-stranded cDNA was
 ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the
 modified p77T3 vector. Library is normalized. Library
 was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 15 a 16 c 18 g 9 t

ORIGIN

Query Match 45.7%; Score 16; DB 9; Length 58;
 Best Local Similarity 68.8%; Pred. No. 3.4e+04;
 Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 atgtctagaatgggagatgggtactctgacc 33
 ||| | ||||| ||||| ||| ||| ||| |||

Db 21 AAGCCCGAATGGGTATGCTTCACCTGCAC 52

Search completed: June 22, 2002, 05:00:13
 Job time: 3273 sec

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74	15.8	43.9	33	6	AX015110	AX015110 Sequence	147	15	41.7	31	6	BD008334	BD008334 Inhibitin
75	15.6	43.3	38	6	I34370	I34370 Sequence 69	148	15	41.7	31	6	E23304	E23304 Antibody ag
76	15.6	43.3	40	6	AX167967	AX167967 Sequence	149	15	41.7	31	6	E27073	E27073 Remedy for
77	15.6	43.3	40	6	BD000227	BD000227 Cell for	150	15	41.7	36	6	A18355	A18355 Oligonucleo
78	15.6	43.3	40	6	BD006861	BD006861 Method fo	151	15	41.7	36	6	AR024287	AR024287 Sequence
79	15.6	43.3	49	6	HSU27250	HSU27250 Human isola	152	15	41.7	36	6	AR045140	AR045140 Sequence
80	15.4	42.8	52	6	165783	165783 Sequence 22	153	15	41.7	36	6	BD011364	BD011364 Chimeric
81	15.4	42.8	33	6	A62591	A62591 Sequence 10	154	15	41.7	36	6	E43834	E43834 Chimeric an
82	15.4	42.8	37	6	AX275051	AX275051 Sequence	155	15	41.7	37	6	AR091832	AR091832 Sequence
83	15.4	42.8	51	6	AX199213	AX199213 Sequence	156	15	41.7	37	6	AR157740	AR157740 Sequence
84	15.4	42.8	51	6	AX199215	AX199215 Sequence	157	15	41.7	38	6	AX068401	AX068401 Sequence
85	15.4	42.8	51	6	AX199493	AX199493 Sequence	158	15	41.7	41	6	AR162657	AR162657 Sequence
86	15.4	42.8	51	6	AX199495	AX199495 Sequence	159	15	41.7	41	6	BD005928	BD005928 Human B-c
87	15.4	42.8	51	6	AX199497	AX199497 Sequence	160	15	41.7	42	6	I15503	I15503 Sequence 4
88	15.4	42.8	66	6	CHRC1A212	CHRC1A212 Sequence	161	15	41.7	44	6	A38860	A38860 Sequence 14
89	15.4	42.8	70	6	E32644	E32644 Method for	162	15	41.7	44	6	A47745	A47745 Sequence 3
90	15.4	42.8	81	14	AF207402	AF207402 Hepatitis	163	15	41.7	44	6	A73049	A73049 Sequence 25
91	15.4	42.8	81	14	AF207403	AF207403 Hepatitis	164	15	41.7	44	6	A73141	A73141 Sequence 25
92	15.4	42.8	81	14	AF207405	AF207405 Hepatitis	165	15	41.7	44	6	AR013765	AR013765 Sequence
93	15.4	42.8	81	14	AF207407	AF207407 Hepatitis	166	15	41.7	44	6	AR093117	AR093117 Sequence
94	15.4	42.8	81	14	AF207408	AF207408 Hepatitis	167	15	41.7	44	6	AR126945	AR126945 Sequence
95	15.4	42.8	81	14	AF207409	AF207409 Hepatitis	168	15	41.7	44	6	AR174690	AR174690 Sequence
96	15.4	42.8	81	14	AF207411	AF207411 Hepatitis	169	15	41.7	50	6	AX199498	AX199498 Sequence
97	15.4	42.8	81	14	AF207412	AF207412 Hepatitis	170	15	41.7	51	6	AX157641	AX157641 Sequence
98	15.4	42.8	81	14	AF207413	AF207413 Hepatitis	171	15	41.7	51	6	AX158719	AX158719 Sequence
99	15.4	42.8	81	14	AF207414	AF207414 Hepatitis	172	15	41.7	51	6	AX158720	AX158720 Sequence
100	15.4	42.8	81	14	AF207415	AF207415 Hepatitis	173	15	41.7	51	6	AX158721	AX158721 Sequence
101	15.4	42.8	81	14	AF207416	AF207416 Hepatitis	174	15	41.7	51	6	AX158722	AX158722 Sequence
102	15.4	42.8	81	14	AF207417	AF207417 Hepatitis	175	15	41.7	55	6	A08730	A08730 Nucleotide
103	15.4	42.8	81	14	AF207418	AF207418 Hepatitis	176	15	41.7	55	6	A08731	A08731 reverse com
104	15.4	42.8	81	14	AF207420	AF207420 Hepatitis	177	15	41.7	55	6	A14751	A14751 Nucleotide
105	15.4	42.8	81	14	AF207421	AF207421 Hepatitis	178	15	41.7	55	6	A14752	A14752 Nucleotide
106	15.4	42.8	81	14	AF207422	AF207422 Hepatitis	179	15	41.7	58	6	A17932	A17932 Oligonucleo
107	15.4	42.8	81	14	AF207423	AF207423 Hepatitis	180	15	41.7	58	6	I24542	I24542 Sequence 22
108	15.4	42.8	81	14	AF207424	AF207424 Hepatitis	181	15	41.7	58	6	I33884	I33884 Sequence 23
109	15.4	42.8	81	14	AF207425	AF207425 Hepatitis	182	15	41.7	58	6	I56779	I56779 Sequence 2
110	15.4	42.8	81	14	AF207426	AF207426 Hepatitis	183	15	41.7	58	6	I83675	I83675 Sequence 4
111	15.4	42.8	81	14	AF207428	AF207428 Hepatitis	184	15	41.7	60	10	MM5HT3B1	MM5HT3B1
112	15.4	42.8	81	14	AF207429	AF207429 Hepatitis	185	15	41.7	98	9	AB032815	AB032815 Homo sapi
113	15.4	42.8	81	14	AF207430	AF207430 Hepatitis	186	14.8	41.1	18	6	A06675	A06675 Oligonucleo
114	15.4	42.8	81	14	AF207431	AF207431 Hepatitis	187	14.8	41.1	18	6	A09099	A09099 Oligonucleo
115	15.4	42.8	81	14	AF207432	AF207432 Hepatitis	188	14.8	41.1	26	6	AR003614	AR003614 Sequence
116	15.4	42.8	81	14	AF207433	AF207433 Hepatitis	189	14.8	41.1	26	6	AR071163	AR071163 Sequence
117	15.4	42.8	81	14	AF207434	AF207434 Hepatitis	190	14.8	41.1	26	6	AR108164	AR108164 Sequence
118	15.4	42.8	81	14	AF207435	AF207435 Hepatitis	191	14.8	41.1	26	6	I22381	I22381 Sequence 7
119	15.4	42.8	81	14	AF207436	AF207436 Hepatitis	192	14.8	41.1	37	6	AX228583	AX228583 Sequence
120	15.4	42.8	81	14	AF207437	AF207437 Hepatitis	193	14.8	41.1	43	6	AR161407	AR161407 Sequence
121	15.4	42.8	81	14	AF207438	AF207438 Hepatitis	194	14.8	41.1	51	6	A00936	A00936 Nucleotide
122	15.4	42.8	81	14	AF207439	AF207439 Hepatitis	195	14.8	41.1	51	6	A00937	A00937 Nucleotide
123	15.4	42.8	81	14	AF207440	AF207440 Hepatitis	196	14.8	41.1	62	6	AR171487	AR171487 Sequence
124	15.4	42.8	81	14	AF207441	AF207441 Hepatitis	197	14.8	41.1	62	6	BD005507	BD005507 Compositi
125	15.4	42.8	89	5	CHRCOLA12	CHRCOLA12 Sequence	198	14.8	41.1	77	10	M05JHCD3	M05JHCD3
126	15.4	42.8	93	6	AX327599	AX327599 Sequence	199	14.8	41.1	98	6	AX287660	AX287660 Sequence
127	15.2	42.2	28	6	AR055231	AR055231 Sequence	200	14.6	40.6	21	6	AX201251	AX201251 Sequence
128	15.2	42.2	35	6	I05643	I05643 Sequence 2	201	14.6	40.6	26	6	AR090181	AR090181 Sequence
129	15.2	42.2	37	6	AX219956	AX219956 Sequence	202	14.6	40.6	28	6	AR054129	AR054129 Sequence
130	15.2	42.2	37	6	AX228614	AX228614 Sequence	203	14.6	40.6	34	6	AX316603	AX316603 Sequence
131	15.2	42.2	47	6	AR070123	AR070123 Sequence	204	14.6	40.6	35	6	AX316601	AX316601 Sequence
132	15.2	42.2	51	6	AX118305	AX118305 Sequence	205	14.6	40.6	38	6	AB8532	AB8532 Sequence 78
133	15.2	42.2	51	6	AX158081	AX158081 Sequence	206	14.6	40.6	38	6	AX088706	AX088706 Sequence
134	15.2	42.2	51	6	AX158083	AX158083 Sequence	207	14.6	40.6	38	6	AX258833	AX258833 Sequence
135	15.2	42.2	51	6	AX159625	AX159625 Sequence	208	14.6	40.6	38	6	AX258836	AX258836 Sequence
136	15.2	42.2	51	6	AX161938	AX161938 Sequence	209	14.6	40.6	39	6	AR123938	AR123938 Sequence
137	15.2	42.2	17	6	BD004410	BD004410 Amelliorat	210	14.6	40.6	44	6	AX305183	AX305183 Sequence
138	15.2	42.2	17	6	BD004466	BD004466 Therapeut	211	14.6	40.6	48	6	AX244175	AX244175 Sequence
139	15.2	42.2	17	6	BD004527	BD004527 Therapeut	212	14.6	40.6	50	6	AX161637	AX161637 Sequence
140	15.2	42.2	17	6	BD008360	BD008360 Inhibitin	213	14.6	40.6	51	6	AX117469	AX117469 Sequence
141	15.2	42.2	17	6	E23330	E23330 Antibody ag	214	14.6	40.6	51	6	AX161995	AX161995 Sequence
142	15.2	42.2	17	6	E27099	E27099 Remedy for	215	14.6	40.6	51	6	AX161996	AX161996 Sequence
143	15.2	42.2	26	6	AX115139	AX115139 Sequence	216	14.6	40.6	80	11	HUM9P950B	HUM9P950B
144	15.2	42.2	31	6	BD004384	BD004384 Amelliorat	217	14.6	40.6	81	14	AB001403	AB001403 Hepatitis
145	15.2	42.2	31	6	BD004440	BD004440 Therapeut	218	14.6	40.6	81	14	AF166574	AF166574 Hepatitis
146	15.2	42.2	31	6	BD004501	BD004501 Therapeut	219	14.6	40.6	81	14	AF166586	AF166586 Hepatitis

220	14.6	40.6	86	6	AR042750	AR042750 Sequence	c 293	14.2	39.4	56	9	HUMNTCOR02	U84641 Human putat
221	14.6	40.6	100	9	AJ8162	AJ008162 Homo sapi	294	14.2	39.4	57	6	A02051	A02051 Artificial
222	14.4	40.0	20	6	AR091863	AR091863 Sequence	295	14.2	39.4	70	14	RE03M2A	J02321 Reovirus se
223	14.4	40.0	25	6	AR157771	AR157771 Sequence	296	14.2	39.4	87	6	A42449	A42449 Sequence 31
c 224	14.4	40.0	225	6	165383	165383 Sequence 6	c 297	14.2	39.4	90	10	RNU76221	U76221 Rattus norv
225	14.4	40.0	30	6	BD004404	BD004404 Ameliorat	298	14.2	39.4	96	6	E05300	E05300 DNA encodin
226	14.4	40.0	30	6	BD004460	BD004460 Therapeut	299	14.2	39.4	99	6	AX050409	AX050409 Sequence
227	14.4	40.0	30	6	BD004521	BD004521 Therapeut	300	14.2	39.4	100	6	AX287667	AX287667 Sequence
228	14.4	40.0	30	6	BD008354	BD008354 Inhibitin	301	14.2	38.9	33	6	A52067	A52067 Sequence 23
229	14.4	40.0	30	6	E23324	E23324 Antibody ag	302	14	38.9	33	6	AR004371	AR004371 Sequence
230	14.4	40.0	30	6	E27093	E27093 Remedy for	303	14	38.9	33	6	AR067676	AR067676 Sequence
231	14.4	40.0	32	6	AR024308	AR024308 Sequence	304	14	38.9	33	6	AR097162	AR097162 Sequence
232	14.4	40.0	32	6	AR045161	AR045161 Sequence	305	14	38.9	33	6	AR130660	AR130660 Sequence
233	14.4	40.0	32	6	AR165166	AR165166 Sequence	306	14	38.9	33	6	AR169821	AR169821 Sequence
234	14.4	40.0	32	6	AX114312	AX114312 Sequence	307	14	38.9	33	6	AR172009	AR172009 Sequence
235	14.4	40.0	32	6	BD011385	BD011385 Chimeric	308	14	38.9	33	6	182846	182846 Sequence 25
236	14.4	40.0	32	6	E43855	E43855 Chimeric an	309	14	38.9	34	6	AK102293	AK102293 Sequence
237	14.4	40.0	33	6	115509	115509 Sequence 4	310	14	38.9	35	6	BD004398	BD004398 Ameliorat
238	14.4	40.0	33	6	189331	189331 Sequence 4	311	14	38.9	35	6	BD004454	BD004454 Therapeut
239	14.4	40.0	36	6	AR024282	AR024282 Sequence	312	14	38.9	35	6	BD004515	BD004515 Therapeut
240	14.4	40.0	36	6	AR045135	AR045135 Sequence	313	14	38.9	35	6	BD008348	BD008348 Inhibitin
241	14.4	40.0	36	6	BD004386	BD004386 Ameliorat	314	14	38.9	35	6	E23318	E23318 Antibody ag
242	14.4	40.0	36	6	BD004442	BD004442 Therapeut	315	14	38.9	35	6	E27087	E27087 Remedy for
243	14.4	40.0	36	6	BD004503	BD004503 Therapeut	c 316	14	38.9	37	6	A18356	A18356 Oligonucleo
244	14.4	40.0	36	6	BD008336	BD008336 Inhibitin	317	14	38.9	37	6	AR091839	AR091839 Sequence
245	14.4	40.0	36	6	BD011359	BD011359 Chimeric	318	14	38.9	37	6	AR157747	AR157747 Sequence
246	14.4	40.0	36	6	E23306	E23306 Antibody ag	319	14	38.9	37	6	AX228606	AX228606 Sequence
247	14.4	40.0	36	6	E27075	E27075 Remedy for	320	14	38.9	38	6	AR016264	AR016264 Sequence
248	14.4	40.0	36	6	E43829	E43829 Chimeric an	321	14	38.9	38	6	AX006415	AX006415 Sequence
249	14.4	40.0	45	6	AX323471	AX323471 Sequence	c 322	14	38.9	40	6	AR042818	AR042818 Sequence
250	14.4	40.0	45	6	134331	134331 Sequence 30	323	14	38.9	40	6	AX224357	AX224357 Sequence
c 251	14.4	40.0	51	6	AX159454	AX159454 Sequence	c 324	14	38.9	40	6	AX224362	AX224362 Sequence
c 252	14.4	40.0	51	6	AX352746	AX352746 Sequence	c 325	14	38.9	41	6	A80778	A80778 Sequence 33
253	14.4	40.0	55	6	AR067956	AR067956 Sequence	c 326	14	38.9	41	6	AX022742	AX022742 Sequence
254	14.4	40.0	55	6	AR078911	AR078911 Sequence	327	14	38.9	41	6	AX077736	AX077736 Sequence
255	14.4	40.0	55	6	AR097705	AR097705 Sequence	328	14	38.9	41	6	AX224360	AX224360 Sequence
c 256	14.4	40.0	59	6	AX326761	AX326761 Sequence	329	14	38.9	42	6	AR016270	AR016270 Sequence
c 257	14.4	40.0	60	6	AR125904	AR125904 Sequence	330	14	38.9	42	6	AX077754	AX077754 Sequence
c 258	14.4	40.0	60	6	124271	124271 Sequence 58	331	14	38.9	42	6	AX077755	AX077755 Sequence
c 259	14.4	40.0	66	9	AF189388	AF189388 Homo sapi	332	14	38.9	43	6	AX301771	AX301771 Sequence
260	14.4	40.0	66	6	AX002785	AX002785 Sequence	333	14	38.9	47	6	AX194988	AX194988 Sequence
261	14.4	40.0	68	6	AX148541	AX148541 Sequence	c 334	14	38.9	50	6	AX194994	AX194994 Sequence
262	14.4	40.0	72	6	A94096	A94096 Sequence 77	c 335	14	38.9	50	6	AX199496	AX199496 Sequence
263	14.4	40.0	72	6	AX011181	AX011181 Sequence	c 336	14	38.9	51	6	AX157962	AX157962 Sequence
c 264	14.4	40.0	74	6	134325	134325 Sequence 24	c 337	14	38.9	51	6	AX190219	AX190219 Sequence
c 265	14.4	40.0	81	14	AF166799	AF166799 Hepatitis	338	14	38.9	54	6	A17931	A17931 Oligonucleo
c 266	14.4	40.0	81	14	AF166800	AF166800 Hepatitis	339	14	38.9	54	6	A38679	A38679 Sequence 10
c 267	14.4	40.0	93	9	HUMRH01	L14658 Human funar	340	14	38.9	54	6	124541	124541 Sequence 21
c 268	14.4	40.0	94	5	AF272967	AF272967 Mastacemb	341	14	38.9	54	6	133883	133883 Sequence 22
c 269	14.4	40.0	94	5	AF272968	AF272968 Mastacemb	342	14	38.9	54	6	156778	156778 Sequence 1
270	14.4	40.0	98	6	AR162990	AR162990 Sequence	343	14	38.9	54	6	183674	183674 Sequence 3
c 271	14.4	40.0	98	6	AR162991	AR162991 Sequence	344	14	38.9	55	6	AR003615	AR003615 Sequence
272	14.2	39.4	23	6	A61986	A61986 Sequence 16	345	14	38.9	55	6	AR071164	AR071164 Sequence
273	14.2	39.4	25	6	AX117172	AX117172 Sequence	346	14	38.9	55	6	AR108165	AR108165 Sequence
274	14.2	39.4	27	6	104405	104405 Sequence 3	347	14	38.9	56	6	122382	122382 Sequence 8
275	14.2	39.4	27	6	104434	104434 Sequence 32	c 348	14	38.9	57	6	AX180944	AX180944 Sequence
c 276	14.2	39.4	29	6	AX183868	AX183868 Sequence	c 349	14	38.9	57	6	101657	101657 Sequence 2
c 277	14.2	39.4	31	6	AX247956	AX247956 Sequence	c 350	14	38.9	66	9	HSU91015	HSU91015 Homo saplen
c 278	14.2	39.4	32	6	A73580	A73580 Sequence 4	c 351	14	38.9	75	8	YSCGTGMA	YSCGTGMA Yeast tRNA-
279	14.2	39.4	33	6	AR104469	AR104469 Sequence	c 352	14	38.9	81	4	BR085646	BR085646 Bos taurus
280	14.2	39.4	33	6	AR104470	AR104470 Sequence	c 353	14	38.9	88	4	BR085646	BR085646 Bos taurus
281	14.2	39.4	36	6	AX004141	AX004141 Sequence	c 354	14	38.9	90	9	S80930	S80930 V alpha 2.1
282	14.2	39.4	40	6	AR162661	AR162661 Sequence	c 355	14	38.9	90	10	RNDRS13	U30811 Rattus norv
283	14.2	39.4	40	6	BD005932	BD005932 Human B-c	c 356	14	38.9	98	6	191504	191504 Sequence 38
284	14.2	39.4	46	6	A98781	A98781 Sequence 14	c 357	14	38.9	100	12	SYNNSAA02	M38611 Synthetic h
285	14.2	39.4	51	6	AX117173	AX117173 Sequence	c 358	13.8	38.3	30	6	AX224739	AX224739 Sequence
286	14.2	39.4	51	6	AX118349	AX118349 Sequence	c 359	13.8	38.3	31	6	A06220	A06220 Synthetic D
c 287	14.2	39.4	51	6	AX158947	AX158947 Sequence	c 360	13.8	38.3	31	6	AX249029	AX249029 Sequence
288	14.2	39.4	51	6	AX161817	AX161817 Sequence	361	13.8	38.3	32	6	AX101289	AX101289 Sequence
289	14.2	39.4	51	6	AX161819	AX161819 Sequence	362	13.8	38.3	36	6	AR055641	AR055641 Sequence
290	14.2	39.4	51	6	AX161821	AX161821 Sequence	363	13.8	38.3	36	6	AR071955	AR071955 Sequence
291	14.2	39.4	51	6	AX161823	AX161823 Sequence	364	13.8	38.3	36	6	105897	105897 Sequence 13
292	14.2	39.4	51	6	AX161824	AX161824 Sequence	365	13.8	38.3	36	6	131786	131786 Sequence 6

C 366	13.8	38.3	37	6	AX228560	AX228560 Sequence	C 439	13.6	37.8	34	6	AX106941	AX106941 Sequence
C 367	13.8	38.3	43	6	AX62205	AX62205 Sequence	C 440	13.6	37.8	34	6	AX137871	AX137871 Sequence
C 368	13.8	38.3	43	6	AX006967	AX006967 Sequence	C 441	13.6	37.8	36	6	A27939	A27939 Primer to 1
C 369	13.8	38.3	45	6	AX022429	AX022429 Sequence	C 442	13.6	37.8	36	6	AR129809	AR129809 Sequence
C 370	13.8	38.3	43	6	I49788	I49788 Sequence	C 443	13.6	37.8	36	6	AX043838	AX043838 Sequence
C 371	13.8	38.3	46	6	AX044483	AX044483 Sequence	C 444	13.6	37.8	36	6	AX081224	AX081224 Sequence
C 372	13.8	38.3	50	6	AR032776	AR032776 Sequence	C 445	13.6	37.8	36	6	AX090374	AX090374 Sequence
C 373	13.8	38.3	50	6	I29516	I29516 Sequence	C 446	13.6	37.8	36	6	E36458	E36458 DNA polymer
C 374	13.8	38.3	50	6	I91190	I91190 Sequence	C 447	13.6	37.8	36	6	I13359	I13359 Sequence
C 375	13.8	38.3	51	6	AX117685	AX117685 Sequence	C 448	13.6	37.8	36	6	I26292	I26292 Sequence
C 376	13.8	38.3	51	6	AX117713	AX117713 Sequence	C 449	13.6	37.8	37	6	AX077740	AX077740 Sequence
C 377	13.8	38.3	51	6	AX190062	AX190062 Sequence	C 450	13.6	37.8	37	6	AX220003	AX220003 Sequence
C 378	13.8	38.3	51	6	AX190064	AX190064 Sequence	C 451	13.6	37.8	37	6	AX223014	AX223014 Sequence
C 379	13.8	38.3	51	6	AX199214	AX199214 Sequence	C 452	13.6	37.8	37	6	AX228541	AX228541 Sequence
C 380	13.8	38.3	51	6	AX199216	AX199216 Sequence	C 453	13.6	37.8	38	6	AX077753	AX077753 Sequence
C 381	13.8	38.3	54	6	AX080406	AX080406 Sequence	C 454	13.6	37.8	39	6	AX077739	AX077739 Sequence
C 382	13.8	38.3	57	6	AX040789	AX040789 Sequence	C 455	13.6	37.8	39	6	AX118782	AX118782 Sequence
C 383	13.8	38.3	60	6	AR028966	AR028966 Sequence	C 456	13.6	37.8	39	6	AX224359	AX224359 Sequence
C 384	13.8	38.3	60	6	AR028967	AR028967 Sequence	C 457	13.6	37.8	40	6	AB4405	AB4405 Sequence
C 385	13.8	38.3	60	6	AR156848	AR156848 Sequence	C 458	13.6	37.8	41	6	BD004387	BD004387 Ameliorat
C 386	13.8	38.3	60	6	AR156849	AR156849 Sequence	C 459	13.6	37.8	41	6	BD004443	BD004443 Therapeut
C 387	13.8	38.3	62	14	HS5TRLE	HS5277 Human cytom	C 460	13.6	37.8	41	6	BD004504	BD004504 Therapeut
C 388	13.8	38.3	73	1	BA1RPO601	M79433 Bacterium T	C 461	13.6	37.8	41	6	BD008337	BD008337 Inhibitin
C 389	13.8	38.3	74	1	FSP1651	X53308 Frankia spe	C 462	13.6	37.8	41	6	E23307	E23307 Antibody ag
C 390	13.8	38.3	74	1	KA1651	X53190 Kibdelospor	C 463	13.6	37.8	41	6	E27076	E27076 Remedy for
C 391	13.8	38.3	74	1	SA1651	X53192 Saccharothr	C 464	13.6	37.8	45	6	AR085458	AR085458 Sequence
C 392	13.8	38.3	75	6	AX252335	AX252335 Sequence	C 465	13.6	37.8	45	6	AR088864	AR088864 Sequence
C 393	13.8	38.3	76	10	AF265802	AF265802 Mus muscu	C 466	13.6	37.8	45	6	AR167338	AR167338 Sequence
C 394	13.8	38.3	79	9	HUMGBB41	K00092 Human chor	C 467	13.6	37.8	45	6	AX100526	AX100526 Sequence
C 395	13.8	38.3	80	6	I34322	I34322 Sequence	C 468	13.6	37.8	45	6	E60002	E60002 Ceramide-b1
C 396	13.8	38.3	81	14	AF166630	AF166630 Hepatitis	C 469	13.6	37.8	45	6	I36721	I36721 Sequence
C 397	13.8	38.3	81	14	AF207406	AF207406 Hepatitis	C 470	13.6	37.8	48	6	A99028	A99028 Sequence
C 398	13.8	38.3	81	14	AF207427	AF207427 Hepatitis	C 471	13.6	37.8	50	6	AX165046	AX165046 Sequence
C 399	13.8	38.3	86	6	AR152216	AR152216 Sequence	C 472	13.6	37.8	51	6	AX115625	AX115625 Sequence
C 400	13.8	38.3	86	6	AX039231	AX039231 Sequence	C 473	13.6	37.8	51	6	AX158082	AX158082 Sequence
C 401	13.8	38.3	86	6	AX039471	AX039471 Sequence	C 474	13.6	37.8	51	6	AX158084	AX158084 Sequence
C 402	13.8	38.3	86	6	AX134829	AX134829 Sequence	C 475	13.6	37.8	51	6	AX158561	AX158561 Sequence
C 403	13.8	38.3	86	6	AX134918	AX134918 Sequence	C 476	13.6	37.8	51	6	AX159626	AX159626 Sequence
C 404	13.8	38.3	86	6	AX135037	AX135037 Sequence	C 477	13.6	37.8	51	6	AX160752	AX160752 Sequence
C 405	13.8	38.3	87	6	AX039233	AX039233 Sequence	C 478	13.6	37.8	51	6	AX161937	AX161937 Sequence
C 406	13.8	38.3	87	6	AX039473	AX039473 Sequence	C 479	13.6	37.8	51	6	AX164880	AX164880 Sequence
C 407	13.8	38.3	87	6	AX134831	AX134831 Sequence	C 480	13.6	37.8	51	6	AX165565	AX165565 Sequence
C 408	13.8	38.3	87	6	AX134920	AX134920 Sequence	C 481	13.6	37.8	51	6	AX204340	AX204340 Sequence
C 409	13.8	38.3	87	6	AX135039	AX135039 Sequence	C 482	13.6	37.8	55	9	HMD4F12M3	HMD4F12M3
C 410	13.8	38.3	96	6	AR152241	AR152241 Sequence	C 483	13.6	37.8	56	6	A36725	A36725 Sequence
C 411	13.6	37.8	20	6	AX182206	AX182206 Sequence	C 484	13.6	37.8	60	6	I04854	I04854 Sequence
C 412	13.6	37.8	21	6	AX097256	AX097256 Sequence	C 485	13.6	37.8	70	9	H006874S03	H006874S03
C 413	13.6	37.8	21	6	AX224361	AX224361 Sequence	C 486	13.6	37.8	74	6	AX277135	AX277135 Sequence
C 414	13.6	37.8	22	6	E32640	E32640 Method for	C 487	13.6	37.8	80	6	AR042778	AR042778 Sequence
C 415	13.6	37.8	24	6	AX119402	AX119402 Sequence	C 488	13.6	37.8	80	14	MCPRNA3A	MCPRNA3A
C 416	13.6	37.8	25	6	AR085680	AR085680 Sequence	C 489	13.6	37.8	81	14	AF168866	AF168866 Sequence
C 417	13.6	37.8	25	6	AX279037	AX279037 Sequence	C 490	13.6	37.8	84	6	AX010625	AX010625 Sequence
C 418	13.6	37.8	28	6	E39126	E39126 Porous flbe	C 491	13.6	37.8	85	6	AX023590	AX023590 Sequence
C 419	13.6	37.8	28	6	E39437	E39437 Hollow flbe	C 492	13.6	37.8	90	6	AX210133	AX210133 Sequence
C 420	13.6	37.8	28	6	E39441	E39441 Fiber carry	C 493	13.6	37.8	90	9	HMDTCRABE	HMDTCRABE
C 421	13.6	37.8	28	6	E41581	E41581 Nucleic aci	C 494	13.6	37.8	100	10	HMBRN2	HMBRN2
C 422	13.6	37.8	28	6	E50121	E50121 Porous holl	C 495	13.6	37.8	100	10	RMO230479	RMO230479
C 423	13.6	37.8	28	6	E59661	E59661 Laminate of	C 496	13.4	37.2	24	6	AR018080	AR018080 Sequence
C 424	13.6	37.8	28	6	E59665	E59665 Laminate of	C 497	13.4	37.2	24	6	AR051920	AR051920 Sequence
C 425	13.6	37.8	28	6	E64338	E64338 Nucleic aci	C 498	13.4	37.2	25	6	AX147164	AX147164 Sequence
C 426	13.6	37.8	32	6	A44587	A44587 Sequence	C 499	13.4	37.2	25	6	E12633	E12633
C 427	13.6	37.8	32	6	A50872	A50872 Sequence	C 500	13.4	37.2	27	6	A65605	A65605 Sequence
C 428	13.6	37.8	32	6	AR075549	AR075549 Sequence	C 501	13.4	37.2	27	6	AR109670	AR109670 Sequence
C 429	13.6	37.8	33	6	E39124	E39124 Porous flbe	C 502	13.4	37.2	28	6	A40136	A40136
C 430	13.6	37.8	33	6	E39435	E39435 Hollow flbe	C 503	13.4	37.2	28	6	AX008134	AX008134 Sequence
C 431	13.6	37.8	33	6	E39439	E39439 Fiber carry	C 504	13.4	37.2	29	6	AX039170	AX039170 Sequence
C 432	13.6	37.8	33	6	E41579	E41579 Nucleic aci	C 505	13.4	37.2	30	6	BD001122	BD001122 Method an
C 433	13.6	37.8	33	6	E50119	E50119 Porous holl	C 506	13.4	37.2	30	6	BD001151	BD001151 Method an
C 434	13.6	37.8	33	6	E59659	E59659 Laminate of	C 507	13.4	37.2	31	6	AR098846	AR098846 Sequence
C 435	13.6	37.8	33	6	E59663	E59663 Nucleic aci	C 508	13.4	37.2	34	6	A40137	A40137 Sequence
C 436	13.6	37.8	33	6	E64336	E64336 Nucleic aci	C 509	13.4	37.2	34	23	E10960	E10960 Primer. 9/2
C 437	13.6	37.8	34	6	A40137	A40137 Sequence	C 510	13.4	37.2	35	11	C75828	C75828 Homo saplen
C 438	13.6	37.8	34	6	A93588	A93588 Sequence	C 511	13.4	37.2	37	6	AR091581	AR091581 Sequence

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516	13.4	37.2	45	6	AX267810	AX267810 Sequence		589	13.2	36.7	41	6	AR061614	AR061614 Sequence
517	13.4	37.2	45	6	AX267811	AX267811 Sequence		590	13.2	36.7	41	6	AR108513	AR108513 Sequence
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521	13.4	37.2	51	6	AX159227	AX159227 Sequence		594	13.2	36.7	41	6	185050	185050 Sequence 29
522	13.4	37.2	51	9	HSA139226	AX132926 Homo sapi		595	13.2	36.7	44	6	AR008958	AR008958 Sequence
523	13.4	37.2	58	6	AR049625	AR049625 Sequence		596	13.2	36.7	44	6	AR013766	AR013766 Sequence
524	13.4	37.2	60	6	AR121644	AR121644 Sequence		597	13.2	36.7	44	6	124412	124412 Sequence 7
525	13.4	37.2	66	6	E55391	E55391 Process for		598	13.2	36.7	45	6	A92629	A92629 Sequence 1
526	13.4	37.2	66	6	AX179470	AX179470 Sequence		599	13.2	36.7	45	6	AR071264	AR071264 Sequence
527	13.4	37.2	69	6	AR052653	AR052653 Sequence		600	13.2	36.7	45	6	AR152959	AR152959 Sequence
528	13.4	37.2	71	6	A60841	A60841 Sequence 15		601	13.2	36.7	45	6	AR160711	AR160711 Sequence
529	13.4	37.2	74	9	S74825	S74825 RET...ELF1		602	13.2	36.7	45	6	AX164014	AX164014 Sequence
530	13.4	37.2	75	8	ECTRNE5U	X05359 E.coli tRNA		603	13.2	36.7	46	6	AX076698	AX076698 Sequence
531	13.4	37.2	76	8	SOBTRFA	M25610 S.obliquus		604	13.2	36.7	46	6	AX076699	AX076699 Sequence
532	13.4	37.2	81	6	A23330	AR013746 Oligonucleo		605	13.2	36.7	46	6	AX076700	AX076700 Sequence
533	13.4	37.2	81	6	AR013746	AR013746 Sequence		606	13.2	36.7	46	6	AX076701	AX076701 Sequence
534	13.4	37.2	81	6	AR174706	AR174706 Sequence		607	13.2	36.7	46	6	AX076702	AX076702 Sequence
535	13.4	37.2	83	4	RABPRKM18	M14473 RabbLc Musc		608	13.2	36.7	46	6	AX076703	AX076703 Sequence
536	13.4	37.2	86	6	AX038232	AX039232 Sequence		609	13.2	36.7	48	6	A18479	A18479 Sequence
537	13.4	37.2	86	6	AX039472	AX039472 Sequence		610	13.2	36.7	48	6	A23087	A23087 Sequence
538	13.4	37.2	86	6	AX134830	AX134830 Sequence		611	13.2	36.7	48	6	A24249	A24249 Sequence
539	13.4	37.2	86	6	AX134919	AX134919 Sequence		612	13.2	36.7	48	6	A24285	A24285 Sequence
540	13.4	37.2	86	6	AX135038	AX135038 Sequence		613	13.2	36.7	48	6	AR028593	AR028593 Sequence
541	13.4	37.2	87	6	AX039234	AX039234 Sequence		614	13.2	36.7	48	6	AR084939	AR084939 Sequence
542	13.4	37.2	87	6	AX039474	AX039474 Sequence		615	13.2	36.7	48	6	AR084955	AR084955 Sequence
543	13.4	37.2	87	6	AX134832	AX134832 Sequence		616	13.2	36.7	48	6	AR085804	AR085804 Sequence
544	13.4	37.2	87	6	AX134921	AX134921 Sequence		617	13.2	36.7	48	6	AX010634	AX010634 Sequence
545	13.4	37.2	87	6	AX135040	AX135040 Sequence		618	13.2	36.7	48	6	E31323	E31323 Process for
546	13.4	37.2	89	6	AR162979	AR162979 Sequence		619	13.2	36.7	48	6	119335	119335 Sequence 33
547	13.4	37.2	92	6	AX209072	AX209072 Sequence		620	13.2	36.7	49	6	HS030447	HS030447 Human Isola
548	13.4	37.2	94	6	AX326633	AX326633 Sequence		621	13.2	36.7	49	6	AX097523	AX097523 Sequence
549	13.4	37.2	94	6	AX326634	AX326634 Sequence		622	13.2	36.7	50	6	AX279653	AX279653 Sequence
550	13.4	37.2	94	6	AX326658	AX326658 Sequence		623	13.2	36.7	50	6	AX156906	AX156906 Sequence
551	13.4	37.2	94	6	AX326671	AX326671 Sequence		624	13.2	36.7	51	6	AX156949	AX156949 Sequence
552	13.4	37.2	100	9	AR8139	AX008139 Homo sapi		625	13.2	36.7	51	6	AX161815	AX161815 Sequence
553	13.2	36.7	18	6	EO6995	EO6995 5'Primer to		626	13.2	36.7	51	6	AX162278	AX162278 Sequence
554	13.2	36.7	19	6	AX130953	AX130953 Sequence		627	13.2	36.7	51	6	AX162635	AX162635 Sequence
555	13.2	36.7	20	6	AR116329	AR116329 Sequence		628	13.2	36.7	51	6	AX163179	AX163179 Sequence
556	13.2	36.7	20	6	AR121479	AR121479 Sequence		629	13.2	36.7	51	6	AX163180	AX163180 Sequence
557	13.2	36.7	20	6	AR121480	AR121480 Sequence		630	13.2	36.7	51	6	AX165117	AX165117 Sequence
558	13.2	36.7	20	6	EO4077	EO4077 Primer for		631	13.2	36.7	51	6	AX198233	AX198233 Sequence
559	13.2	36.7	22	6	143046	143046 Sequence 29		632	13.2	36.7	51	6	AX198233	AX198233 Sequence
560	13.2	36.7	24	6	E13472	E13472 PCR Primer		633	13.2	36.7	51	6	AX199234	AX199234 Sequence
561	13.2	36.7	27	6	AR040342	AR040342 Sequence		634	13.2	36.7	51	6	105584	105584 Sequence 15
562	13.2	36.7	27	6	E12636	E12636 DNA Oligome		635	13.2	36.7	52	6	AX150268	AX150268 Sequence
563	13.2	36.7	30	6	A02053	AR024327 Artificial		636	13.2	36.7	55	6	106069	106069 Sequence 16
564	13.2	36.7	30	6	AR024327	AR024327 Sequence		637	13.2	36.7	56	6	106070	106070 Sequence 17
565	13.2	36.7	30	6	AR045180	AR045180 Sequence		638	13.2	36.7	56	12	SYNPLECA	SYNPLECA
566	13.2	36.7	30	6	AX100545	AX100545 Sequence		639	13.2	36.7	57	6	A02005	A02005 Artificial
567	13.2	36.7	30	6	BD011404	BD011404 Chimeric		640	13.2	36.7	57	6	A06451	A06451 Artificial
568	13.2	36.7	30	6	E43874	E43874 Chimeric an		641	13.2	36.7	58	6	AR055542	AR055542 Sequence
569	13.2	36.7	31	6	AR048182	AR048182 Sequence		642	13.2	36.7	58	6	AR082726	AR082726 Sequence
570	13.2	36.7	31	6	AX135237	AX135237 Sequence		643	13.2	36.7	58	6	AR084868	AR084868 Sequence
571	13.2	36.7	31	6	AX151286	AX151286 Sequence		644	13.2	36.7	58	6	AR087676	AR087676 Sequence
572	13.2	36.7	32	6	A08190	A08190 Oligonucleo		645	13.2	36.7	58	6	AR094036	AR094036 Sequence
573	13.2	36.7	32	6	E31942	E31942 Seven-pass		646	13.2	36.7	60	6	AR028968	AR028968 Sequence
574	13.2	36.7	33	6	AR100744	AR100744 Sequence		647	13.2	36.7	60	6	AR028969	AR028969 Sequence
575	13.2	36.7	33	6	AR125614	AR125614 Sequence		648	13.2	36.7	60	6	AR156850	AR156850 Sequence
576	13.2	36.7	33	6	AR130199	AR130199 Sequence		649	13.2	36.7	60	6	AR156851	AR156851 Sequence
577	13.2	36.7	36	6	AX094463	AX094463 Sequence		650	13.2	36.7	60	6	AE011614	AE011614 Homo sapi
578	13.2	36.7	36	6	AX009719	AX009719 Sequence		651	13.2	36.7	60	9	AR171489	AR171489 Sequence
579	13.2	36.7	36	6	BD007707	BD007707 Dioxin re		652	13.2	36.7	62	6	BD005509	BD005509 Compositi
580	13.2	36.7	36	6	BD007709	BD007709 Dioxin re		653	13.2	36.7	62	6	105585	105585 Sequence 16
581	13.2	36.7	37	6	AX219949	AX219949 Sequence		654	13.2	36.7	64	6	144603	144603 Sequence 32
582	13.2	36.7	37	6	AX220081	AX220081 Sequence		655	13.2	36.7	64	6	171008	171008 Sequence
583	13.2	36.7	37	6	AX220122	AX220122 Sequence		656	13.2	36.7	64	8	AF129578	AF129578 Racomilitri
584	13.2	36.7	37	6	AX228613	AX228613 Sequence		657	13.2	36.7	64	8		

C 658	13.2	36.7	66	0	104136	Sequence 24	731	13	36.1	32	6	AX137632	AX137632 Sequence
C 659	13.2	36.7	67	6	AR061632	Sequence	733	13	36.1	33	6	AX326580	AX326580 Sequence
C 660	13.2	36.7	67	6	AR108531	Sequence	733	13	36.1	34	6	AR065602	AR065602 Sequence
C 661	13.2	36.7	67	6	AX286215	Sequence	734	13	36.1	34	6	AR065614	AR065614 Sequence
C 662	13.2	36.7	67	6	116488	Sequence 31	735	13	36.1	36	6	AR018937	AR018937 Sequence
C 663	13.2	36.7	67	6	166974	Sequence 31	736	13	36.1	36	6	AR065655	AR065655 Sequence
C 664	13.2	36.7	67	6	185068	Sequence 31	737	13	36.1	36	6	172282	172282 Sequence 64
C 665	13.2	36.7	74	3	DME426972	Drosophila	738	13	36.1	36	6	176849	176849 Sequence 64
C 666	13.2	36.7	74	6	AX089704	Sequence	739	13	36.1	37	6	AX219933	AX219933 Sequence
C 667	13.2	36.7	74	6	AX090159	Sequence	740	13	36.1	37	6	AX220095	AX220095 Sequence
C 668	13.2	36.7	74	6	SS9798517	Sequence	741	13	36.1	38	6	AX350544	AX350544 Sequence
C 669	13.2	36.7	75	6	A20281	PKLR-L-type	742	13	36.1	38	6	E36560	E36560 Vector for
C 670	13.2	36.7	75	6	A20282	oligonucleo	743	13	36.1	39	6	AR026875	AR026875 Sequence
C 671	13.2	36.7	77	9	HSSRCE9	oligonucleo	744	13	36.1	39	6	AR049301	AR049301 Sequence
C 672	13.2	36.7	80	11	DM164C3T	Human c-src	745	13	36.1	39	6	AR065559	AR065559 Sequence
C 673	13.2	36.7	81	6	A20283	771123 D. melanoga	746	13	36.1	39	6	AR118111	AR118111 Sequence
C 674	13.2	36.7	81	14	AF221161	A20283 oligonucleo	747	13	36.1	39	10	MM2299475	MM2299475 Mus muscu
C 675	13.2	36.7	81	14	AF221163	Hepatitis	748	13	36.1	41	6	AR127573	AR127573 Sequence
C 676	13.2	36.7	81	14	AF221165	Hepatitis	749	13	36.1	42	6	A27187	A27187 Oligonucleo
C 677	13.2	36.7	81	14	AF221165	Hepatitis	750	13	36.1	42	6	AR058955	AR058955 Sequence
C 678	13.2	36.7	81	14	AF221409	Hepatitis	751	13	36.1	42	6	AR105229	AR105229 Sequence
C 679	13.2	36.7	82	6	AR175473	Sequence	752	13	36.1	42	6	AR119150	AR119150 Sequence
C 680	13.2	36.7	82	6	AR175474	Sequence	753	13	36.1	42	6	AR123521	AR123521 Sequence
C 681	13.2	36.7	82	6	AR175475	Sequence	754	13	36.1	42	6	AR138174	AR138174 Sequence
C 682	13.2	36.7	84	6	AR041032	Sequence	755	13	36.1	42	6	AR176735	AR176735 Sequence
C 683	13.2	36.7	84	9	AF312274	Homo sapi	756	13	36.1	42	6	AX300421	AX300421 Sequence
C 684	13.2	36.7	85	4	OCT90	Rabbit trop	757	13	36.1	42	10	MMTCRBEF4	MMTCRBEF4 X70761 M. musculus
C 685	13.2	36.7	85	10	MMV156X1	269822 M.musculus	758	13	36.1	43	6	AR050860	AR050860 Sequence
C 686	13.2	36.7	85	10	RATRS1	K00370 Rat Ser-trn	759	13	36.1	43	6	E07917	E07917 Synthetic D
C 687	13.2	36.7	85	10	RNTNSER	X02685 Rat (BUF) t	760	13	36.1	46	6	E12821	E12821 PCR primer
C 688	13.2	36.7	86	6	AR140846	Sequence	761	13	36.1	46	6	E12821	E12821 PCR primer
C 689	13.2	36.7	86	6	AR150796	Sequence	762	13	36.1	48	6	AR012090	AR012090 Sequence
C 690	13.2	36.7	86	6	165674	Sequence 34	763	13	36.1	48	6	AR014529	AR014529 Sequence
C 691	13.2	36.7	86	6	167906	Sequence 34	764	13	36.1	49	5	CI1HBABA	CI1HBABA Duck alpha-
C 692	13.2	36.7	86	6	190127	Sequence 34	765	13	36.1	49	6	AB3164	AB3164 Sequence 14
C 693	13.2	36.7	89	6	114150	Sequence 31	766	13	36.1	51	6	AX118301	AX118301 Sequence
C 694	13.2	36.7	91	6	196194	Sequence 31	767	13	36.1	51	6	AX156901	AX156901 Sequence
C 695	13.2	36.7	91	6	H0MSRC08	K03215 Human c-src	768	13	36.1	51	6	AX156903	AX156903 Sequence
C 696	13.2	36.7	92	6	AR041029	Sequence	769	13	36.1	51	6	AX156905	AX156905 Sequence
C 697	13.2	36.7	93	6	AX023591	Sequence	770	13	36.1	51	6	AX158956	AX158956 Sequence
C 698	13.2	36.7	93	9	HSU39141	Human r cel	771	13	36.1	51	6	AX161377	AX161377 Sequence
C 699	13.2	36.7	94	5	AY005394	Chysemys	772	13	36.1	51	6	AX161862	AX161862 Sequence
C 700	13.2	36.7	94	5	AY005396	Chysemys	773	13	36.1	51	6	AX162435	AX162435 Sequence
C 701	13.2	36.7	94	5	AY005397	Chysemys	774	13	36.1	51	6	AX164879	AX164879 Sequence
C 702	13.2	36.7	94	5	AY005398	Chysemys	775	13	36.1	51	6	AX165574	AX165574 Sequence
C 703	13.2	36.7	94	5	AY005399	Cynops or	776	13	36.1	51	6	AX190216	AX190216 Sequence
C 704	13.2	36.7	96	9	SS3463	Homo sapien	777	13	36.1	54	9	HS4224301	HS4224301 Homo sapi
C 705	13.2	36.7	97	6	114149	Sequence 1	778	13	36.1	54	23	E09579	E09579 DNA encodin
C 706	13.2	36.7	98	6	AX287656	Sequence	779	13	36.1	55	6	A63661	A63661 Sequence 27
C 707	13.2	36.7	98	6	AX287662	Sequence	780	13	36.1	57	9	HS422485	HS422485 Homo sapi
C 708	13.2	36.7	98	9	H0MTPS4	M22378 Human trans	781	13	36.1	57	9	SS2911	SS2911 TCR alpha V
C 709	13.2	36.7	98	12	SYN1INA	118417 Synthetic H	782	13	36.1	57	10	AF328240	AF328240 Mus muscu
C 710	13.2	36.7	100	9	H0MCH1P05	113324 Homo sapien	783	13	36.1	64	6	AR160127	AR160127 Sequence
C 711	13	36.1	15	6	185762	Sequence 1	784	13	36.1	65	6	A60851	A60851 Sequence 16
C 712	13	36.1	19	6	A07386	Nucleotide	785	13	36.1	65	6	156698	156698 Sequence 14
C 713	13	36.1	19	6	A14843	Nucleotide	786	13	36.1	65	23	E09583	E09583 Linker. 9/2
C 714	13	36.1	21	6	AR058934	Sequence	787	13	36.1	68	6	AX258830	AX258830 Sequence
C 715	13	36.1	21	6	AX249727	Sequence	788	13	36.1	69	6	AR016616	AR016616 Sequence
C 716	13	36.1	24	6	AX288715	Sequence	789	13	36.1	69	6	115349	115349 Sequence 30
C 717	13	36.1	24	6	AX327692	Sequence	790	13	36.1	70	6	AR077330	AR077330 Sequence
C 718	13	36.1	24	6	BD000509	Protein,	791	13	36.1	70	6	AR123765	AR123765 Sequence
C 719	13	36.1	25	6	165382	Sequence 5	792	13	36.1	72	6	AX089389	AX089389 Sequence
C 720	13	36.1	25	6	E13691	PCR primer	793	13	36.1	72	6	AR081359	AR081359 Sequence
C 721	13	36.1	27	6	AR039746	Sequence	794	13	36.1	75	6	AR166410	AR166410 Sequence
C 722	13	36.1	27	6	BD003097	Polynucle	795	13	36.1	75	6	119526	119526 Sequence 3
C 723	13	36.1	28	6	AR091086	Sequence	796	13	36.1	75	6	186206	186206 Sequence 3
C 724	13	36.1	28	6	AX025073	Sequence	797	13	36.1	75	9	AF043756	AF043756 Homo sapi
C 725	13	36.1	28	6	AX025095	Sequence	798	13	36.1	75	23	E09581	E09581 Linker. 9/2
C 726	13	36.1	28	6	BD001912	Remedy of	799	13	36.1	79	6	AX233527	AX233527 Sequence
C 727	13	36.1	30	6	AX202306	Sequence	800	13	36.1	80	5	U93455	U93455 Scyllorhinu
C 728	13	36.1	31	6	AR041195	Sequence	801	13	36.1	81	9	S60067	S60067 T-cell anti
C 729	13	36.1	31	6	AR116604	Sequence	802	13	36.1	81	14	AB001398	AB001398 Hepatitis
C 730	13	36.1	31	6	AR159947	Sequence	803	13	36.1	81	14	AB001414	AB001414 Hepatitis

804	13	36.1	81	14	AF16589	AF16589 Hepatitis	C 877	12.8	35.6	44	6	AR110226	AR110226 Sequence
805	13	36.1	81	14	AF207465	AF207465 Hepatitis	C 878	12.8	35.6	44	6	AR110237	AR110237 Sequence
806	13	36.1	81	14	AF207468	AF207468 Hepatitis	C 879	12.8	35.6	44	6	AR110239	AR110239 Sequence
807	13	36.1	81	14	AF207469	AF207469 Hepatitis	C 880	12.8	35.6	44	6	AR169883	AR169883 Sequence
808	13	36.1	81	14	AF207470	AF207470 Hepatitis	C 881	12.8	35.6	44	6	AR169885	AR169885 Sequence
809	13	36.1	81	14	AF207471	AF207471 Hepatitis	C 882	12.8	35.6	44	6	AR169966	AR169966 Sequence
810	13	36.1	81	14	AF207472	AF207472 Hepatitis	C 883	12.8	35.6	44	6	AR169998	AR169998 Sequence
811	13	36.1	81	14	AF207473	AF207473 Hepatitis	C 884	12.8	35.6	44	6	AR171792	AR171792 Sequence
812	13	36.1	81	14	AF207474	AF207474 Hepatitis	C 885	12.8	35.6	44	6	AR171794	AR171794 Sequence
813	13	36.1	81	14	AF207476	AF207476 Hepatitis	C 886	12.8	35.6	44	6	AR171805	AR171805 Sequence
814	13	36.1	81	14	AF207477	AF207477 Hepatitis	C 887	12.8	35.6	44	6	AR171807	AR171807 Sequence
815	13	36.1	81	14	AF207478	AF207478 Hepatitis	C 888	12.8	35.6	44	6	BD009017	BD009017 Promoter
816	13	36.1	81	14	AF207479	AF207479 Hepatitis	C 889	12.8	35.6	44	6	BD009019	BD009019 Promoter
817	13	36.1	81	14	AF207480	AF207480 Hepatitis	C 890	12.8	35.6	44	6	BD009030	BD009030 Promoter
C 818	13	36.1	84	6	AF7942	AF7942 Sequence 57	C 891	12.8	35.6	44	6	BD009032	BD009032 Promoter
C 819	13	36.1	84	6	E17278	E17278 Primer, 7/1	C 892	12.8	35.6	44	6	E12782	E12782 DNA probe f
C 820	13	36.1	87	6	AR081443	AR081443 Sequence	C 893	12.8	35.6	45	6	AR110245	AR110245 Sequence
C 821	13	36.1	87	6	AR081512	AR081512 Sequence	C 894	12.8	35.6	45	6	AR170004	AR170004 Sequence
C 822	13	36.1	90	6	AR152211	AR152211 Sequence	C 895	12.8	35.6	45	6	AR171813	AR171813 Sequence
C 823	13	36.1	90	6	AR152236	AR152236 Sequence	C 896	12.8	35.6	45	6	AX343783	AX343783 Sequence
C 824	13	36.1	93	6	A42846	A42846 Sequence 17	C 897	12.8	35.6	45	6	BD009038	BD009038 Promoter
C 825	13	36.1	93	6	I87352	I87352 Sequence 17	C 898	12.8	35.6	45	6	ES2011	ES2011 IL-6 recept
C 826	13	36.1	94	6	AX023633	AX023633 Sequence	C 899	12.8	35.6	47	6	A38861	A38861 Sequence 15
C 827	13	36.1	94	10	MUSIGAPCI	M32003 Mus musculu	C 900	12.8	35.6	47	6	A38864	A38864 Sequence 18
C 828	13	36.1	95	6	AX080110	AX080110 Sequence	C 901	12.8	35.6	47	6	A48403	A48403 Sequence 26
C 829	13	36.1	95	6	AX080111	AX080111 Sequence	C 902	12.8	35.6	47	6	A73050	A73050 Sequence 26
C 830	13	36.1	95	11	G31168	G31168 UC-49 Human	C 903	12.8	35.6	47	6	A73052	A73052 Sequence 28
C 831	13	36.1	96	6	AX088792	AX088792 Sequence	C 904	12.8	35.6	47	6	A73142	A73144 Sequence 26
C 832	13	36.1	96	6	AR052009	AR052009 Sequence	C 905	12.8	35.6	47	6	A73144	A73144 Sequence 28
C 833	13	36.1	99	9	S73910	S73910 TCR alpha V	C 906	12.8	35.6	47	6	AR126946	AR126946 Sequence
C 834	13	36.1	100	11	HSAS250606	AJ250606 Homo sapi	C 907	12.8	35.6	47	6	AR126948	AR126948 Sequence
C 835	12.8	35.6	18	6	AX098721	AX098721 Sequence	C 908	12.8	35.6	47	6	AR174691	AR174691 Sequence
C 836	12.8	35.6	20	6	AR084408	AR084408 Sequence	C 909	12.8	35.6	47	6	AR174693	AR174693 Sequence
C 837	12.8	35.6	20	6	AX058354	AX058354 Sequence	C 910	12.8	35.6	50	6	I07020	I07020 Sequence 2
C 838	12.8	35.6	20	6	AX058355	AX058355 Sequence	C 911	12.8	35.6	50	6	I07025	I07025 Sequence 7
C 839	12.8	35.6	20	6	AX062314	AX062314 Sequence	C 912	12.8	35.6	50	6	I27622	I27622 Sequence 14
C 840	12.8	35.6	20	6	AX062315	AX062315 Sequence	C 913	12.8	35.6	50	6	I27627	I27627 Sequence 19
C 841	12.8	35.6	20	6	AX292982	AX292982 Sequence	C 914	12.8	35.6	51	6	AX115749	AX115749 Sequence
C 842	12.8	35.6	20	6	E16974	E16974 PCR primer	C 915	12.8	35.6	51	6	AX157106	AX157106 Sequence
C 843	12.8	35.6	24	6	AX117463	AX117463 Sequence	C 916	12.8	35.6	51	6	AX158339	AX158339 Sequence
C 844	12.8	35.6	24	6	AX288349	AX288349 Sequence	C 917	12.8	35.6	51	6	AX158340	AX158340 Sequence
C 845	12.8	35.6	24	6	E63259	E63259 Fused prote	C 918	12.8	35.6	51	6	AX159170	AX159170 Sequence
C 846	12.8	35.6	25	6	AX043517	AX043517 Sequence	C 919	12.8	35.6	51	6	AX165234	AX165234 Sequence
C 847	12.8	35.6	26	6	BD007197	BD007197 Method an	C 920	12.8	35.6	51	6	AX199161	AX199161 Sequence
C 848	12.8	35.6	27	6	A07875	A07875 Oligonucleo	C 921	12.8	35.6	52	6	AX017168	AX017168 Sequence
C 849	12.8	35.6	30	6	AX180271	AX180271 Sequence	C 922	12.8	35.6	52	6	E08119	E08119 Synthetic D
C 850	12.8	35.6	30	6	I44798	I44798 Sequence 22	C 923	12.8	35.6	54	6	ES2010	ES2010 IL-6 recept
C 851	12.8	35.6	31	6	AX249666	AX249666 Sequence	C 924	12.8	35.6	55	6	AR008947	AR008947 Sequence
C 852	12.8	35.6	32	6	AR107549	AR107549 Sequence	C 925	12.8	35.6	55	6	BD004798	BD004798 Novel pol
C 853	12.8	35.6	34	6	I25954	I25954 Sequence 7	C 926	12.8	35.6	55	6	I27102	I27102 Sequence 18
C 854	12.8	35.6	36	6	AR031680	AR031680 Sequence	C 927	12.8	35.6	55	23	E09673	E09673 PCR primer
C 855	12.8	35.6	36	6	I90298	I90298 Sequence 40	C 928	12.8	35.6	56	6	AR032988	AR032988 Sequence
C 856	12.8	35.6	37	6	AX220102	AX220102 Sequence	C 929	12.8	35.6	56	6	I29728	I29728 Sequence 60
C 857	12.8	35.6	37	6	AX228601	AX228601 Sequence	C 930	12.8	35.6	56	6	I91402	I91402 Sequence 60
C 858	12.8	35.6	37	6	AX228616	AX228616 Sequence	C 931	12.8	35.6	57	6	AX320858	AX320858 Sequence
C 859	12.8	35.6	38	6	AR156817	AR156817 Sequence	C 932	12.8	35.6	57	10	MMU90454	MMU90454 Mus musculu
C 860	12.8	35.6	39	6	AR013768	AR013768 Sequence	C 933	12.8	35.6	59	6	A80777	A80777 Sequence 32
C 861	12.8	35.6	39	6	AX209950	AX209950 Sequence	C 934	12.8	35.6	59	6	AR009036	AR009036 Sequence
C 862	12.8	35.6	39	6	AX209958	AX209958 Sequence	C 935	12.8	35.6	59	6	AR011160	AR011160 Sequence
C 863	12.8	35.6	40	6	AR031988	AR031988 Sequence	C 936	12.8	35.6	59	6	AR052691	AR052691 Sequence
C 864	12.8	35.6	40	6	AX025066	AX025066 Sequence	C 937	12.8	35.6	59	6	AR175124	AR175124 Sequence
C 865	12.8	35.6	40	6	AX025088	AX025088 Sequence	C 938	12.8	35.6	59	6	AX022741	AX022741 Sequence
C 866	12.8	35.6	40	6	AX055762	AX055762 Sequence	C 939	12.8	35.6	59	6	AX023613	AX023613 Sequence
C 867	12.8	35.6	42	6	AR021417	AR021417 Sequence	C 940	12.8	35.6	59	6	I17798	I17798 Sequence 27
C 868	12.8	35.6	42	6	AR042979	AR042979 Sequence	C 941	12.8	35.6	59	6	I74710	I74710 Sequence 50
C 869	12.8	35.6	42	6	AR161282	AR161282 Sequence	C 942	12.8	35.6	60	6	I34343	I34343 Sequence 42
C 870	12.8	35.6	42	6	I43961	I43961 Sequence 50	C 943	12.8	35.6	60	10	AF265815	AF265815 Mus muscu
C 871	12.8	35.6	42	6	I62970	I62970 Sequence 67	C 944	12.8	35.6	62	6	AR092480	AR092480 Sequence
C 872	12.8	35.6	42	6	I88723	I88723 Sequence 67	C 945	12.8	35.6	62	6	AR117204	AR117204 Sequence
C 873	12.8	35.6	43	6	A04411	A04411 Oligonucleo	C 946	12.8	35.6	62	9	AB010672	AB010672 Homo sapi
C 874	12.8	35.6	43	6	AR003318	AR003318 Sequence	C 947	12.8	35.6	68	6	AR092479	AR092479 Sequence
C 875	12.8	35.6	44	6	AR049103	AR049103 Sequence	C 948	12.8	35.6	68	6	AR117203	AR117203 Sequence
C 876	12.8	35.6	44	6	AR110224	AR110224 Sequence	C 949	12.8	35.6	69	9	S78642	S78642 19 VH3A10-I

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C 950 12.8 35.6 70 3 TF28SRNAB 218236 Triticohomo
C 951 12.8 35.6 73 6 ARI29049 Sequence
C 952 12.8 35.6 73 6 ARI29049 Sequence
C 953 12.8 35.6 73 6 E17115 Oligonucleo
C 954 12.8 35.6 73 6 E17115 Linker. 7/1
C 955 12.8 35.6 73 6 E26013 Clamydia tr
C 956 12.8 35.6 73 6 E32123 Soluble fus
C 957 12.8 35.6 75 6 E16727 Oligonucleo
C 958 12.8 35.6 75 6 E17116 Linker. 7/1
C 959 12.8 35.6 75 6 E26014 Clamydia tr
C 960 12.8 35.6 75 6 E32124 Soluble fus
C 961 12.8 35.6 76 11 H0MT7883A tr
C 962 12.8 35.6 78 3 AVO133989
C 963 12.8 35.6 78 6 A37066 Drosophila
C 964 12.8 35.6 78 6 A37067 Sequence 9
C 965 12.8 35.6 78 6 A37067 Sequence 10
C 966 12.8 35.6 79 6 ARI26057 Human mRNA
C 967 12.8 35.6 80 14 ARI26057 Mus muscu
C 968 12.8 35.6 81 14 D00305 Wheat dwarf
C 969 12.8 35.6 81 14 AFO18362 Hepatitis
C 970 12.8 35.6 83 6 AFI66791 Hepatitis
C 971 12.8 35.6 83 6 AX240981 Sequence
C 972 12.8 35.6 83 6 AX241021 Sequence
C 973 12.8 35.6 84 11 AGRPD25T7
C 974 12.8 35.6 87 10 AFO41877 Mus muscu
C 975 12.8 35.6 87 10 M28227 Mouse activ
C 976 12.8 35.6 89 6 AX046263 Sequence
C 977 12.8 35.6 89 6 AX046264 Sequence
C 978 12.8 35.6 89 6 S77398S1 CYP11B2-ste
C 979 12.8 35.6 90 6 I49792 Sequence 15
C 980 12.8 35.6 90 6 HUMABP M15532 Human amylo
C 981 12.8 35.6 95 9 Z99561 Homo sapien
C 982 12.8 35.6 96 3 AB015654 Plasmodiu
C 983 12.8 35.6 96 3 L42794 Homo sapien
C 984 12.8 35.6 97 10 AF230479 Mus muscu
C 985 12.8 35.6 98 6 I42296 Sequence 10
C 986 12.8 35.6 98 6 AJO05152 Homo sapi
C 987 12.8 35.6 100 6 ARI28598 Sequence
C 988 12.8 35.6 100 6 G43568 WIAF-2436-S
C 989 12.6 35.0 20 6 AX188409 Sequence
C 990 12.6 35.0 20 6 AX293348 Sequence
C 991 12.6 35.0 21 6 A50871 A50871 Sequence 4
C 992 12.6 35.0 21 6 ARI62021 Sequence
C 993 12.6 35.0 21 6 AX201227 Sequence
C 994 12.6 35.0 22 6 AX134191 Sequence
C 995 12.6 35.0 22 11 HOMO11LB D50256 A PCR prime
C 996 12.6 35.0 23 6 I49664 D59644 Sequence 6
C 997 12.6 35.0 23 6 E09345 Oligonucleo
C 998 12.6 35.0 23 6 E09648 Oligonucleo
C 999 12.6 35.0 23 6 E11796 DNA fragmen
C1000 12.6 35.0 24 6 ARO22191 Sequence
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ALIGNMENTS

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RESULT 1
AX299123 65 bp DNA linear PAT 26-NOV-2001
LOCUS AX299123
DEFINITION Sequence 6 from Patent WO0183528.
ACCESSION AX299123
VERSION AX299123.1 GI:17129032
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (sites)
AUTHORS Haynes,J.R., Macklin,M.D. and Payne,L.G.
TITLE Nucleic acid immunization
JOURNAL Patent: WO 0183528-A 6 08-NOV-2001;
FEATURES
Location/Qualifiers
Source 1..65
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Construct"
BASE COUNT 20 a 20 c 14 g 11 t
ORIGIN
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Query Match 55.0%; Score 19.8; DB 6; Length 65;
Best Local Similarity 77.4%; Pred. No. 2.7e+03;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 5 aaagctccacatgagcagacccaagt 35
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Db 4 AAAGCTCCACATGAGCTTCTAACCGAGT 34
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RESULT 2
AR091831 34 bp DNA linear PAT 07-SEP-2000
LOCUS AR091831
DEFINITION Sequence 30 from patent US 5994524.
ACCESSION AR091831
VERSION AR091831.1 GI:10018585
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 34)
AUTHORS Matsushima,K., Matsumoto,Y., Yamada,Y., Sato,K., Tsuchiya,M. and
Yamazaki,T.
TITLE Polynucleotides which encode reshaped IL-8-specific antibodies and
methods to produce the same
JOURNAL Patent: US 5994524-A 30 30-NOV-1999;
FEATURES
Location/Qualifiers
Source 1..34
BASE COUNT 9 a 10 c 7 g 8 t
ORIGIN
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Query Match 53.3%; Score 19.2; DB 6; Length 34;
Best Local Similarity 75.0%; Pred. No. 5.1e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 4 aaagctccacatgagcagacccaagt 35
|||||
Db 3 AAAGCTCCACATGAGTGTCTCACTCAGT 34
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RESULT 3
AR157739 34 bp DNA linear PAT 17-OCT-2001
LOCUS AR157739
DEFINITION Sequence 30 from patent US 6245894.
ACCESSION AR157739
VERSION AR157739.1 GI:16218746
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 34)
AUTHORS Matsushima,K., Matsumoto,Y., Yamada,Y., Sato,K., Tsuchiya,M. and
Yamazaki,T.
TITLE Reshaped human antibody to human interleukin-8
JOURNAL Patent: US 6245894-A 30 12-JUN-2001;
FEATURES
Location/Qualifiers
Source 1..34
BASE COUNT 9 a 10 c 7 g 8 t
ORIGIN
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Query Match 53.3%; Score 19.2; DB 6; Length 34;
Best Local Similarity 75.0%; Pred. No. 5.1e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Qy 4 aaagcttcacatgagccagacccaagt 35
|||||
Db 3 AAAGCTTCACCATGATGTGCTCACTCAGG 34

RESULT 4
AR171488
LOCUS Sequence 14 from patent US 6297048. 55 bp DNA linear PAT 17-DEC-2001
DEFINITION AR171488
ACCESSION AR171488
VERSION AR171488.1 GI:17910438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 55)
AUTHORS Jolly,D., Chang,S.M.W., Lee,W.T.L., Townsend,K. and O'Dea,J.
TITLE Hepatitis therapeutics
JOURNAL Patent: US 6297048-A 14 02-OCT-2001;
FEATURES
source 1..55
location/Qualifiers
BASE COUNT 25 a 16 c 6 g 8 t
ORIGIN

Query Match 51.7%; Score 18.6; DB 6; Length 55;
Best Local Similarity 72.7%; Pred. No. 8.4e+03;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 gcgaagcttcacatgagccagacccaag 33
|||||
Db 3 GCTTAAGCTTCACCATGACGACAAATCTTAA 35

RESULT 5
BD005508
LOCUS BD005508 55 bp DNA linear PAT 31-JAN-2002
DEFINITION BD005508
ACCESSION BD005508
VERSION BD005508.1 GI:18633879
KEYWORDS JP 2001500738-A/14.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 55)
AUTHORS Saliberg,M., Milich,D.R. and Lee,W.T.L.
TITLE Compositions and methods for treating intracellular diseases.
JOURNAL Patent: JP 2001500738-A 14 23-JAN-2001;
COMMENT CHIRON CORP. THE SCRIPPS RESEARCH INSTITUTE
OS Unidentified
PN JP 2001500738-A/14
PD 23-JAN-2001
PF 16-SEP-1997 JP 1998514832
PR
PI MATTI SALIBERG,DAVID R MILICH,WILLIAM T L LEE PC
C12N15/36,C12N15/19,A61K48/00,A61K39/12,A61K39/29 CC
Strandedness: Single;
CC Topology: Linear;
FH Key
FT source 1..55
location/Qualifiers
BASE COUNT 25 a 16 c 6 g 8 t
ORIGIN

Query Match 51.7%; Score 18.6; DB 6; Length 55;
Best Local Similarity 72.7%; Pred. No. 8.4e+03;

Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 gcgaagcttcacatgagccagacccaag 33
|||||
Db 3 GCTTAAGCTTCACCATGACGACAAATCTTAA 35

RESULT 6
AX326742
LOCUS AX326742 75 bp DNA linear PAT 07-JAN-2002
DEFINITION AX326742
ACCESSION AX326742
VERSION AX326742.1 GI:18097468
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Zauderer,M. and Smith,E.S.
TITLE Methods of producing a library and methods of selecting
JOURNAL polynucleotides of interest
UNIVERSITY OF ROCHESTER (US)
location/Qualifiers
FEATURES
source 1..75
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleotide Sequence of PEU/TK"
BASE COUNT 19 a 16 c 19 g 21 t
ORIGIN

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Best Local Similarity 74.2%; Pred. No. 1.2e+04;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 40 AAAGCGCGCGCATGTGGCCGCCGCCCAACG 70

RESULT 7
AX275053
LOCUS AX275053 36 bp DNA linear PAT 29-OCT-2001
DEFINITION AX275053
ACCESSION AX275053
VERSION AX275053.1 GI:16547657
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Thomson,A.R., Liu,B. and Danilenko,D.M.
TITLE Fibroblast growth factor-like polypeptides
JOURNAL Patent: WO 0118172-A 12 15-MAR-2001;
Amgen Inc., (US)
location/Qualifiers
FEATURES
source 1..36
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 10 a 12 c 8 g 6 t
ORIGIN

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Best Local Similarity 80.8%; Pred. No. 1.6e+04;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 cgaaagcttcacatgagccagac 27
|||||
Db 4 CTTAAGCTTCACCATGACGACCTCGAC 29

RESULT 8
LOCUS A63737 48 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 1 from Patent WO9723613.
ACCESSION A63737
VERSION A63737.1 GI:3717315
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 48)
AUTHORS Bebbington,C.R., Lawson,A.D., Weir,A.N. and Finney,H.M.
TITLE CELL ACTIVATION PROCESS AND REAGENTS THEREFOR
JOURNAL Patent: WO 9723613-A 1 03-JUL-1997;
CELLTECH THERAPEUTICS LTD (GB)
COMMENT Other publication AU 120197 19970717.
FEATURES
SOURCE location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 10 a 20 c 8 g 10 t
ORIGIN

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Best Local Similarity 70.6%; Pred. No. 1.5e+04;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 cgaagcttcacatgagcagacccaagt 35
|||
Db 11 ccgaagcttcacatgagcagacccaagt 44

RESULT 9
LOCUS A36805 82 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 24 from Patent EP0589840.
ACCESSION A36805
VERSION A36805.1 GI:2294071
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 82)
AUTHORS Hardman,N., Kolbinger,F. and Saldanha,J.
TITLE Reshaped monoclonal antibodies against an immunoglobulin isotype
JOURNAL Patent: EP 0589840-A 24 30-MAR-1994;
CTBA GEIGY AG (CH)
COMMENT Other publication JP 6225788 940816
Other publication NZ 248743 950427
Other publication CN 1088986 940706
Other publication CA 2106719 940325
Other publication AU 4748893 940331
Other publication ZA 9307033 940811
Other publication NO 933394 940325
Other publication FI 934145 940325.
FEATURES
SOURCE location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 11 a 23 c 23 g 25 t
ORIGIN

Query Match 50.0%; Score 18; DB 6; Length 82;
Best Local Similarity 80.8%; Pred. No. 1.4e+04;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 11 ccacatgagccagacccaagt 36
|||||
Db 60 CCACCTTCGGCCAGGCGCACCAAGTG 35

RESULT 10
LOCUS AR075883/C 82 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 24 from patent US 5958708.
ACCESSION AR075883
VERSION AR075883.1 GI:10002629
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 82)
AUTHORS Hardman,N., Kolbinger,F. and Saldanha,J.
TITLE Reshaped monoclonal antibodies against an immunoglobulin isotype
JOURNAL Patent: US 5958708-A 24 28-SEP-1999;
FEATURES
SOURCE location/Qualifiers
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/organism="unknown"
BASE COUNT 11 a 23 c 23 g 25 t
ORIGIN

Query Match 50.0%; Score 18; DB 6; Length 82;
Best Local Similarity 80.8%; Pred. No. 1.4e+04;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 11 ccacatgagccagacccaagt 36
|||||
Db 60 CCACCTTCGGCCAGGCGCACCAAGTG 35

RESULT 11
LOCUS AR097672/C 82 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 24 from patent US 6072035.
ACCESSION AR097672
VERSION AR097672.1 GI:12806402
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 82)
AUTHORS Hardman,N., Kolbinger,F. and Saldanha,J.
TITLE Reshaped monoclonal antibodies against an immunoglobulin isotype
JOURNAL Patent: US 6072035-A 24 06-JUN-2000;
FEATURES
SOURCE location/Qualifiers
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/organism="unknown"
BASE COUNT 11 a 23 c 23 g 25 t
ORIGIN

Query Match 50.0%; Score 18; DB 6; Length 82;
Best Local Similarity 80.8%; Pred. No. 1.4e+04;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 11 ccacatgagccagacccaagt 36
|||||
Db 60 CCACCTTCGGCCAGGCGCACCAAGTG 35

RESULT 12
LOCUS AX277694 36 bp DNA linear PAT 01-NOV-2001
DEFINITION Sequence 1 from Patent WO0177681.
ACCESSION AX277694
VERSION AX277694.1 GI:16604839
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (sites)
AUTHORS Waring,R.D. and Phoenix,J.

/db_xref="taxon:11103"
 /clone="P3"
 /note="Isolated from patient NR4"
 genotype: 3"
 <1..>81
 /note="hypervariable region 1"
 <1..>81
 /codon_start=1
 /product="polyprotein"
 /protein_id="AAD52450.1"
 /db_xref="GI:5815007"
 /translation="NRYTGGAMAHGARGITSLFVSGPKON"

BASE COUNT 21 a 21 c 20 g 19 t
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Query Match 48.9%; Score 17.6; DB 14; Length 81;
 Best Local Similarity 83.3%; Pred. No. 2e+04; 4; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 ctccaccatgagccagcacca 31
 || |||||
 Db 41 CTGGCAACCATGAGCATGCGACCA 18

Search completed: June 22, 2002, 05:31:51
 Job time: 5071 sec

C 959	13	36.1	51	22	AAH40628	Human SNP flanking
C 960	13	36.1	51	23	ABL00083	Human silent nonco
C 961	13	36.1	51	23	ABL00778	Human amino acid c
C 962	13	36.1	53	21	AAZ58956	Primer for constru
C 963	13	36.1	54	16	AAO95955	Signal sequence fo
C 964	13	36.1	55	18	AAT93324	Primer #1 for glyc
C 965	13	36.1	59	18	AAV79360	Staphylococcus aur
C 966	13	36.1	61	21	AAA89748	Mouse ECD-PD fusio
C 967	13	36.1	64	16	AAQ97219	Modified hlt-3 sig
C 968	13	36.1	64	18	AAT99298	Modified sequence
C 969	13	36.1	64	21	AAA03763	Modified human int
C 970	13	36.1	65	16	AAQ99612	Mouse Ah receptor
C 971	13	36.1	65	18	AAT85446	5' primer OL-68 am
C 972	13	36.1	65	19	AAV54301	Primer JMTCR2 used
C 973	13	36.1	65	20	AAZ55383	Soluble sc-TCR fus
C 974	13	36.1	66	20	AAZ77738	Human ConvL1 oligo
C 975	13	36.1	66	20	AAZ76096	Light chain consen
C 976	13	36.1	70	22	AAZ00077	Human Interferon b
C 977	13	36.1	70	22	AAZ29243	Ligand to CD40 lig
C 978	13	36.1	71	15	AAQ57942	Hepatitis A virus
C 979	13	36.1	72	13	AAQ33954	Downstream sequenc
C 980	13	36.1	72	20	AAZ59220	PCR primer CR508 u
C 981	13	36.1	73	19	AAV55420	Interleukin-3 sign
C 982	13	36.1	73	20	AAZ59218	PCR primer CR503 u
C 983	13	36.1	74	21	AAZ52804	MB83 heavy chain
C 984	13	36.1	75	15	AAQ55730	DNA ligase Oligo A
C 985	13	36.1	75	17	AAT14927	Oligo A template f
C 986	13	36.1	75	20	AAZ77739	Human ConvL1 oligo
C 987	13	36.1	75	20	AAZ76097	Light chain consen
C 988	13	36.1	76	14	AAQ49814	IL-3 signal sequen
C 989	13	36.1	77	22	ABA73545	Human foetal liver
C 990	13	36.1	77	22	ABA38820	Probe #17286 for g
C 991	13	36.1	77	22	AAK21991	Human brain expres
C 992	13	36.1	77	22	AAK48154	Human bone marrow
C 993	13	36.1	77	22	AAT26143	Probe #16076 for g
C 994	13	36.1	77	22	AAI53984	Probe #22670 used
C 995	13	36.1	79	22	AAZ43708	Cornedoesmosin sin
C 996	13	36.1	81	22	AAK45635	Human bone marrow
C 997	13	36.1	81	22	AAI51566	Probe #20252 used
C 998	13	36.1	83	22	ABA70427	Human foetal liver
C 999	13	36.1	83	22	ABA71599	Human foetal liver
C1000	13	36.1	83	22	ABA37076	Probe #15542 for g

ALIGNMENTS

RESULT 1

ID AAT70936 standard; DNA; 65 BP.

XX	AAI70936;
AC	12-MAR-2002 (first entry)
XX	
DT	Influenza virus M2 antigen 5' PCR primer.
XX	
DE	Vaccine: M2 protein; antigen; nucleic acid immunisation; Cpg;
XX	adjuvant; PCR primer; ss.
KW	Influenza virus type A.
XX	Synthetic.
OS	
OS	WO200183528-A2.
PN	
XX	
PD	08-NOV-2001.
XX	
PF	01-MAY-2001; 2001WO-GB01924.
XX	
PR	01-MAY-2000; 2000US-200968P.
PR	01-MAY-2000; 2000US-0561951.
PR	08-JUN-2000; 2000US-210580P.
XX	

PA (POWD-) POWDERJECT VACCINES INC.
PA (POWD-) POWDERJECT RES LTD.
XX
PI Haynes JR, Macklin MD, Payne LG;
XX WPI; 2002-041480/05.

XX Use of nucleic acid sequence which encodes influenza virus M2 antigen
XX and which is not present in a recombinant viral vector, for manufacture
XX of medicament for vaccination against an influenza virus -
XX
XX Example 1; Page 37; 69pp; English.

XX The present sequence is that of a 5' PCR primer (3' primer given
XX on AAT70937) used in the PCR amplification of DNA encoding the
XX M2 antigen of influenza virus strain A/Sydney/5/97 (H3N2). In
XX addition to M2-derived sequences, the 5' primer contains additional
XX 5' sequences that include a recognition site for HindIII and a Kozak
XX consensus sequence to facilitate mRNA translation initiation. The
XX PCR product was used in the construction of vaccine vector plasmid
XX PM2-FL (see AAT70939). A claimed polynucleotide vaccine
XX composition comprises a nucleic acid sequence that encodes the M2
XX antigen (see AAM50534-36) of a type A influenza virus, and which is
XX not present in a recombinant viral vector. Upon introduction
XX to a subject, the nucleic acid sequence is expressed to provide the
XX influenza virus M2 antigen in an amount sufficient to elicit an
XX immune response.

SO Sequence 65 BP; 20 A; 20 C; 14 G; 11 T; 0 other;

Query Match 55.0%; Score 19.8; DB 24; Length 65;
Best Local Similarity 77.4%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 5 aagcttcacccatgagccagacacaaagt 35
Db 4 aagcttcacccatgagccatcaccgaggt 34

RESULT 2

ID AAT16940 standard; DNA; 34 BP.

XX	AAT16940;
AC	19-SEP-1996 (first entry)
XX	
DT	Murine anti-human IL-8 MAB light V region cDNA PCR primer cHVL.
XX	
DE	Variable; light chain; WS4; hybridoma; monoclonal; pUC-WS4-VL;
XX	antibody; MAB; BALB/c mouse; spleen cell; human; interleukin-8;
KW	IL-8; myeloma P3X63-Ag8.653 cell; CDR; framework; chimeric
KW	complementarity determining region; chimeric; murine; PCR;
KW	inflammation; disease; mediated; low antigenicity; primer;
KW	polymerase chain reaction; ss.
XX	Synthetic.
OS	
OS	WO9602576-A1.
PN	
XX	
PD	01-FEB-1996.
XX	
PF	12-JUL-1995; 95WO-JP01396.
XX	
PR	14-DEC-1994; 94JP-0310785.
PR	13-JUL-1994; 94JP-0161481.
PR	24-NOV-1994; 94JP-0289951.
XX	
PA	(CHUS) CHUGAI SEIYAKU KK.
XX	
XX	Matsumoto Y, Matsushima K, Sato K, Tsuchiya M, Yamada Y;
PI	Yamazaki T;

```
XX DR WPI; 1996-105864/11.
XX XX
PT Reconstituted human antibody recognising human interleukin-8
PT containing mouse anti-IL8 antibody variable region sequences, has
PT low antigenicity in humans
XX XX
PS Example 4; Page 73; 125pp; Japanese.
XX XX
CC The present sequence is a PCR primer for pUC-WS4-VL, which encodes
CC the variable light chain from a WS4 hybridoma monoclonal antibody
CC (Mab). The hybridoma was constructed by fusing BALB/c mouse spleen
CC cells, immunised with human IL-8, with mouse myeloma P3X63-Ag8.653
CC cells. Complementarity determining region (CDR) DNA from pUC-WS4-VL
CC and its heavy chain equivalent pUC-WS4-VH, was used together with
CC human framework region DNA to construct chimeric H and L region, V
CC region DNA. The DNA was then inserted into a HEF vector along with
CC human C-kappa and C-gamma-1, C region DNA to produce a vector
CC capable of expressing a human/murine chimaeric Mab. The Mab can be
CC used for the treatment of inflammatory diseases mediated by IL-8,
CC and as the major part of the Mab comes from a human Ab, and only
CC the CDR regions are of murine origin, the Mab has the advantage of
CC having low antigenicity to the human body when used
CC therapeutically.
CC XX
SQ Sequence 34 BP; 9 A; 10 C; 7 G; 8 T; 0 other;

Query Match 53.3%; Score 19.2; DB 17; Length 34;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4 aaagctccaccatgacgcagacccaagt 35
Db 3 aaagctccaccatgacgcagacccaagt 34

RESULT 3
AAT09869
ID AAT09869 standard; cDNA; 38 BP.
XX AC AAT09869;
XX DT 15-OCT-1996 (first entry)
XX XX
DE Human neurotransmitter transporter protein 5' DNA primer.
XX XX
KW Neurotransmitter transporter protein; pain therapy; stroke therapy;
KW amyotrophic lateral sclerosis; oligonucleotide; DNA primer; PCR;
KW polymerase chain reaction; ss.
XX OS Synthetic.
XX PN WO9531539-A1.
XX XX
PD 23-NOV-1995.
XX XX
PE 16-MAY-1994; 94WO-US05363.
XX XX
PR 16-MAY-1994; 94WO-US05363.
PR 26-MAY-1994; 94ZA-0003696.
XX XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
PI Fleischmann RD, Li Y;
XX DR WPI; 1996-010925/01.
XX XX
PT DNA encoding neuro:transmitter transporter protein and related
PT (ant)agonists - useful to treat e.g., amyotrophic lateral sclerosis,
PT pain and stroke.
XX XX
PS Disclosure: Page 32; 53pp; English.
```

```
XX XX
CC This 5' primer is used in the construction of a plasmid for
CC expression of recombinant NRT in COS cells. This primer contains
CC a BglII site followed by 21 nucleotide of NRT coding sequence
CC starting from the initiation codon.
CC XX
SQ Sequence 38 BP; 14 A; 10 C; 9 G; 5 T; 0 other;

Query Match 51.7%; Score 18.6; DB 17; Length 38;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 4 aaagctccaccatgacgcagacccaagt 36
Db 6 agatctgcaccatgacgcagacccaagt 38

RESULT 4
AAQ47027
ID AAQ47027 standard; DNA; 55 BP.
XX AC AAQ47027;
XX DT 31-JAN-1994 (first entry)
XX DE HCV core sequence isolation primer #4.
XX XX
KW Precore; core; coding region; hepatitis B; virus; HBV; plasmid; PCR;
KW PCR; isolation; HCV; NANBH; non-A, non-B hepatitis; primers; mutation;
KW cytotoxic T-lymphocyte; CTL; PCR; HXHCVcore; hepatitis C; infection;
KW hepatocellular carcinomas; class-I; ss.
XX OS Synthetic.
XX PN WO9315207-A.
XX XX
PD 05-AUG-1993.
XX XX
PE 04-FEB-1993; 93WO-US01009.
XX XX
PR 04-FEB-1992; 92US-0830417.
XX XX
PA (VIAG-) VIAGENE INC.
XX XX
PI Chang SMW, Jolly DJ, Lee WT, O'Dea J, Townsend K;
XX DR WPI; 1993-258682/32.
XX XX
PT Treatment of hepatitis B and C, and associated carcinoma(s) -
PT using a vector construct directing the expression of part of
PT hepatitis B or C antigen
XX XX
PS Example 2C; Page 29; 110pp; English.
XX XX
CC The sequences given in AAQ47024-29 are primers which were used in the
CC isolation of the core coding region of hepatitis C virus (HCV). The
CC viral DNA which was used as a template in the PCR reaction, was
CC isolated from serum obtained from a patient with chronic non-A,
CC non-B hepatitis (NANBH). Three separate PCR reactions were performed
CC in the production of a 570 bp amplification product. This oligomer
CC was ligated into the pCRII vector and designated PCR1H-XHCVcore.
CC The isolated HCV core region may be used in a method to induce potent
CC class-I restricted protective and therapeutic cytotoxic T-lymphocyte
CC (CTL) response, and a humoral response for the treatment of hepatitis
CC B and C infections, as well as hepatocellular carcinomas.
XX XX
SQ Sequence 55 BP; 25 A; 16 C; 6 G; 8 T; 0 other;

Query Match 51.7%; Score 18.6; DB 14; Length 55;
Best Local Similarity 72.7%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

Qy 1 gcgaaagcttcacatgagccagacaccaa 33
11 | | | | | | | | | | | | | | | | | |
Db 3 gcttaagcttcacatgagccacaaatcctaa 35

RESULT 5

AAV30020
ID AAV30020 standard; DNA; 55 BP.

AC AAV30020;

DT 13-AUG-1998 (first entry)

DE PCR primer used to amplify a Hepatitis C virus core sequence.

KW HCV core sequence; treatment; intracellular infection; mammal;

KW immunogenic portion; antigen; intracellular pathogen;

KW bacterial infection; legionella; tuberculosis; chlamydia;

KW parasitic infection; rickettsia; leishmaniasis; malaria; viral infection;

KW Herpes; HIV; FIV; PCR primer; ss.

XX Synthetic.

OS Hepatitis C virus.

XX WO9812332-A1.

PD 26-MAR-1998.

XX 16-SEP-1997; 97WO-US16453.

XX 17-SEP-1996; 96US-0025267.

XX (CHIR) CHIRON CORP.

PA (SCRI) SCRIPPS RES. INST.

XX Lee WTL, Milich DR, Salberg M;

XX WPI: 1998-217270/19.

DR Vector construct directing expression of intracellular pathogenic

XX antigen - useful for, e.g. treatment of intracellular diseases in

PT animals such as tuberculosis and chlamydia

XX Example 2; Page 35; 141pp; English.

XX PCR primers AAV30020-21 were used to amplify a Hepatitis C virus (HCV)

XX core sequence, using as a template the amplification product of

XX primers AAV30016-17. Two consecutive stop codons are added in frame with

XX the HCV gene. The amplified product is cloned and used to exemplify

XX the invention, which describes a method for treating intracellular

XX infections of warm-blooded mammals. This comprises administering to the

XX mammal a vector construct which directs the expression of at least one

XX immunogenic portion of an antigen derived from an intracellular pathogen

XX (e.g. HBV), and also administering a protein which comprises the

XX immunogenic portion of the antigen. The composition is used to treat

XX intracellular infections within warm-blooded animals e.g. bacterial

XX infections such as legionella, tuberculosis and chlamydia, parasitic

XX infections such as rickettsia, leishmaniasis or malaria and viral

XX infections like Hepatitis, Herpes, HIV and FIV.

XX Sequence 55 BP; 25 A; 16 C; 6 G; 8 T; 0 other;

Query Match 51.7%; Score 18.6; DB 19; Length 55;

Best Local Similarity 72.7%; Pred. No. 2e+02; Mismatches 9; Indels 0; Gaps 0;

Qy 1 gcgaaagcttcacatgagccagacaccaa 33
11 | | | | | | | | | | | | | | | | | |
Db 3 gcttaagcttcacatgagccacaaatcctaa 35

RESULT 6
AAD21201
ID AAD21201 standard; DNA; 55 BP.

AC AAD21201;

DT 15-JAN-2002 (first entry)

DE Sense PCR primer #8 used in the isolation of HCV core sequence.

KW Hepatitis B; hepatitis C; immunogen; HBV; HCV; hepatocellular carcinoma;

KW HCC; gene therapy; virucide; hepatotropic; antiinflammatory; cytostatic;

KW site-directed mutagenesis; PCR primer; ss.

XX Hepatitis C virus.

OS US6297048-B1.

XX 02-OCT-2001.

XX 07-JUN-1995; 95US-0483511.

XX 04-FEB-1992; 92US-0830417.

XX 17-MAR-1993; 93US-0032385.

XX 04-AUG-1993; 93US-0102132.

XX 05-AUG-1994; 94US-0286829.

XX 19-JAN-1995; 95US-0374414.

XX (CHIR) CHIRON CORP.

XX Jolly DJ, Chang SMW, Lee WTL, Townsend K, O'Dea J;

XX WPI: 2001-647290/74.

DR New vectors that direct the (co-)expression of one or more immunogenic

XX portions of the hepatitis B or C virus antigen(s), useful in gene

XX therapy, e.g. for treating or preventing hepatitis B or C infections,

XX or hepatocellular carcinomas

XX Example 2; Column 23; 64pp; English.

XX The present invention relates to a method for treating hepatitis B or C

XX infections. The method involves administering a vector construct that

XX directs the expression of at least one immunogenic portion of hepatitis

XX B virus (HBV) antigen, containing HBeAg, HbCag, HbSag, S, Pre-S1, Pre-S2,

XX open reading frame (ORF) 5, ORF 6, HBV pol or HBxAg or co-expression of

XX at least one immunogenic portion of a HBV antigen and at least one

XX immunogenic portion of a hepatitis C virus (HCV) antigen. The vectors are

XX useful in gene therapy, particularly for treating or preventing

XX hepatitis B and hepatitis C infections, as well as hepatocellular

XX carcinomas (HCC). The present sequence is a PCR primer used in the

XX isolation of HCV core sequence.

XX Sequence 55 BP; 25 A; 16 C; 6 G; 8 T; 0 other;

Query Match 51.7%; Score 18.6; DB 22; Length 55;

Best Local Similarity 72.7%; Pred. No. 2e+02; Mismatches 9; Indels 0; Gaps 0;

Qy 1 gcgaaagcttcacatgagccagacaccaa 33
11 | | | | | | | | | | | | | | | | | |
Db 3 gcttaagcttcacatgagccacaaatcctaa 35

RESULT 7
AAAI5233
ID AAI5233 standard; DNA; 75 BP.

AC AAI5233;

XX 04-SEP-2000 (first entry)

XX

DE Nucleotide sequence of a fragment of the plasmid pE/Ltk.
XX
XX Plasmid pE/Ltk: E/L promoter; thymidine kinase gene; epitope;
KW tumour specific epitope; antigen; vaccine; tumour regression; cancer;
KW infection; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1..51
FT promoter /tag- a
FT /note- "E/L promoter"
FT 52..75
FT misc_feature /tag- b
FT /note- "beginning of the thymidine kinase gene"
XX
XX WO200028016-A1.
XX
XX 18-MAY-2000.
PD
XX 10-NOV-1998; 98WO-US24029.
PF
XX 10-NOV-1998; 98WO-US24029.
PR
XX (UVRP) UNIV ROCHESTER.
PA
XX
PI Zauderer M;
XX
XX WPI: 2000-376533/32.
DR
XX Novel method of identifying target epitopes or antigens specific for
PT human tumors, cancers and infected cells involving screening expression
PT library products of a cell expressing the target epitope -
XX
XX
PS Disclosure: Fig 1; 132pp; English.
XX
XX The present sequence represents a fragment of the plasmid p7.5tk,
CC comprising the E/L promoter and the beginning of the thymidine kinase
CC gene. The pE/Ltk plasmid was used in the course of the invention. The
CC specification describes a method for identifying a target epitope.
CC The method comprises screening the products of an expression library
CC from a cell expressing the target epitope with cytotoxic T cells
CC generated against the cell to identify DNA clones expressing the target
CC epitope. The method may also comprise providing a cytotoxic T cell
CC specific for a gene product differentially expressed by a cell and
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
CC useful for identifying tumour specific target epitopes and antigens which
CC are useful in immunogenic compositions or vaccines to induce the
CC regression of tumors, cancers or infections in mammals. The genes
CC expressed in a panel of tumour cells that are derived from single
CC immortalised, non-tumourigenic cell line are used to generate HLA
CC restricted cytotoxic T cells which are evaluated for activity against
CC tumour cells. The method is useful to identify potential antigens
CC expressed not only by the pathogen but also by the host cells whose gene
CC expression is altered as a result of infection. The differential gene
CC expression strategies can be applied to identify immunogenic molecules
CC of cells infected with virus, fungus or mycobacterium.
XX
XX Sequence 75 BP; 19 A; 16 C; 19 G; 21 T; 0 other:
SQ

Query Match 50.6%; Score 18.2; DB 21; Length 75;
Best Local Similarity 74.2%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 aaagctccacatgagccagacaccaag 34
||||| || ||||| ||| || ||||| |
Db 40 aaagcgccgcacatgagccgcgcgcacag 70

RESULT 8
ABAO1475
ID ABAO1475 standard; DNA; 75 BP.

XX
XX ABAO1475;
AC
XX
XX 04-FEB-2002 (first entry)
DT
XX
XX Partial pE/Ltk sequence.
DE
XX
XX Cell death; toxic gene; tumour suppressor; ds.
KW
XX
XX Synthetic.
OS
XX
XX WO200172995-A2.
PN
XX
XX 04-OCT-2001.
PD
XX
XX 28-MAR-2001; 2001WO-US09953.
PF
XX
XX 28-MAR-2000; 2000US-0192586.
PR
XX 10-MAY-2000; 2000US-0203343.
PR 23-JAN-2001; 2001US-0263226.
PR 27-FEB-2001; 2001US-0271426.
XX
XX (UVRP) UNIV ROCHESTER.
PA
XX
PI Zauderer M, Smith BS;
XX
XX WPI: 2001-570897/64.
DR
XX
XX Selecting target polynucleotides, particularly toxic genes, involves
PT introducing a library of insert polynucleotides into a host cell
PT population, where the target polynucleotide promotes cell death -
XX
XX
PS Disclosure: Fig 1; 359pp; English.
XX
XX The present invention relates to a method for selecting a target
CC polynucleotide. The method comprises introducing into a host cell
CC population a library of insert polynucleotides, where expression of the
CC target polynucleotide directly or indirectly promotes host cell death.
CC The cells are cultured and the insert polynucleotides are collected from
CC the cells which die. The method is useful for selecting target
CC polynucleotides, particularly polynucleotides which alter cell phenotypes
CC of induce or inhibit cell death. The method can be used to isolate toxic
CC genes such as tumour suppressors. The present sequence was used to
CC illustrate the method of the present invention.
XX
XX Sequence 75 BP; 19 A; 16 C; 19 G; 21 T; 0 other:
SQ

Query Match 50.6%; Score 18.2; DB 22; Length 75;
Best Local Similarity 74.2%; Pred. No. 3.1e+02;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 aaagctccacatgagccagacaccaag 34
||||| || ||||| ||| || ||||| |
Db 40 aaagcgccgcacatgagccgcgcgcacag 70

RESULT 9
AAS00786
ID AAS00786 standard; DNA; 36 BP.
XX
XX
XX AAS00786;
AC
XX
XX 24-MAY-2001 (first entry)
DT
XX
XX Human Fibroblast Growth Factor-1like (FGF-1like) DNA PCR primer #2.
DE
XX
XX Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;
KW inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis;
KW renal tubule damage; gastrointestinal abnormality; wasting syndrome; ss;
KW neurodegenerative disease; haematopoietic cell reconstruction; cachexia;
KW chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy;
KW multiple sclerosis; short stature; delayed maturation; excessive growth;
KW

KW	acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia;
KW	androgen target organ abnormality; respiratory distress syndrome; stroke;
KW	cancer; atherosclerosis; hypercholesterolemia; osteoporosis; baldness;
KW	osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue;
KW	decreased stamina; decreased cardiac function; immune system dysfunction;
KW	Parkinson's disease; Alzheimer's disease; decreased cognitive function;
KW	senile dementia; human; PCR primer.
XX	
OS	Homo sapiens.
XX	
PN	WO200118172-A2.
XX	
PD	15-MAR-2001.
XX	
PF	05-SEP-2000; 2000WO-US24373.
XX	
PR	07-SEP-1999; 99US-0391861.
XX	
PR	23-AUG-2000; 2000US-0644052.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Thomason AR, Liu B;
XX	
DR	WPI: 2001-226743/23.
XX	
PT	Novel isolated fibroblast growth factor-like polypeptide useful for
PT	treating, preventing or ameliorating cirrhosis, inflammatory bowel
PT	disease, mucositis, Crohn's disease, diabetes, obesity, stroke and
PT	osteoporosis -
XX	
PS	Example 3; Page 85; 138pp; English.
XX	
CC	The sequence represents a PCR primer used to clone a DNA encoding a human
CC	fibroblast growth factor-like (FGF-like) polypeptide. FGF-like protein
CC	and its associated nucleic acid play a role in modulating body growth,
CC	maturation or life-span. They are also useful for treating, preventing or
CC	ameliorating disorders such as cirrhosis, inflammatory bowel disease,
CC	mucositis, Crohn's disease, diabetes, obesity, gastrointestinal
CC	abnormalities, neurodegenerative diseases, damage to renal tubules as a
CC	result of acute tubular necrosis, haematopoietic cell reconstitution
CC	following chemotherapy, wasting syndromes (e.g., cancer associated
CC	cachexia), damage to the corneal epithelium, lens or retinal tissue,
CC	multiple sclerosis, myopathies, short stature, delayed maturation,
CC	excessive growth (e.g. acromegaly), premature maturation, alopecia,
CC	abnormalities of androgen target organs, bronchopulmonary dysplasia,
CC	acute respiratory distress syndrome, tumours of the eye or other tissues,
CC	atherosclerosis, hypercholesterolemia, stroke, osteoporosis,
CC	osteoarthritis, muscle atrophy, sarcopenia, baldness, wrinkles, increased
CC	fatigue, decreased stamina, decreased cardiac function, immune system
CC	dysfunction, cancer, Parkinson's disease, senile dementia, Alzheimer's
CC	disease, and decreased cognitive function.
XX	
SQ	Sequence 36 BP; 10 A; 12 C; 8 G; 6 T; 0 other;
XX	
Query Match	50.0%; Score 18; DB 22; Length 36;
Best Local Similarity	80.8%; Pred. No. 3.3e+02;
Matches 21; Conservative	0; Mismatches 5; Indels 0;
Gaps 0;	
2Y	2 cgaagcttcaccatgagccagac 27
DB	
4	ctaagcttcaccatgagcgcac 29
RESULT 10	
AAT90515	
ID	AAT90515 standard; DNA; 48 BP.
AC	AAT90515;
XX	
DT	12-FEB-1998 (first entry)
XX	
DE	Human CTMO1 antibody PCR primer R6490.

XX		Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv;
KM		human; cancer; therapy; PCR; primer; ss.
XX		Synthetic.
OS		Homo sapiens.
XX		WO9723613-A2.
PN		03-JUL-1997.
XX		23-DEC-1996;
PF		96WO-GB03209.
XX		21-DEC-1995;
PR		95GB-0026131.
XX		(CLIT) CELLTech THERAPEUTICS LTD.
PA		Bebington CR, Finney HM, Lawson ADG, Weir ANC;
XX		WPI, 1997-351052/32.
DR		New DNA systems for activating cells - comprising DNA coding for a
PT		chimeric receptor comprising 2 or more different cytoplasmic
PT		signalling components.
XX		Example 1; Fig 3; 90pp; English.
PS		Primer R6490 was used with primer R6516 (see AAT90516) in the PCR
XX		cloning of the leader sequence and VL region of human anti-CD3
CC		antibody CTMO1. R6490 introduces 5' NotI and HindIII sites and
CC		R6515 forms part of a (GlyAser)5 linker. The leader-VL fragment
CC		was spliced to a VH fragment and subcloned into pluscript SK+ to
CC		form a CTMO1 scFv cassette. This can be utilised in novel chimeric
CC		genes (see AAT90509-14) encoding recombinant chimeric receptors (see
CC		AAT26646-51) useful in cell activation processes, e.g. for the
CC		treatment of cancer.
SO		Sequence 48 BP; 10 A; 20 C; 8 G; 10 T; 0 other;
QY		Query Match 50.0%; Score 18; DB 18; Length 48;
		Best Local Similarity 70.6%; Pred. No. 3.5e+02;
Matches	24; Conservative	0; Mismatches 10; Indels 0; Gaps 0;
OY	2 cgaagcttcacacatgagcagcacccaagt 35	
DB	11 cgcaagcttcacacatgtctgcaccaccaagt 44	
RESULT 11		
AAV41509/C		
ID	AAV41509 standard; DNA; 53 BP.	
XX		
AC	AAV41509;	
XX		
DT	24-SEP-1998 (first entry)	
XX		
DE	Nucleotide sequence of PCR primer HCV.	
XX		
KW	Ribozyme; substrate S2; low magnesium condition; cleavage; PCR;	
KW	target RNA; bacterial infection; viral infection; HIV; primer;	
XX	RNA-specific restriction endonuclease; amplification; ss.	
OS	Synthetic.	
XX		
PN	WO9743404-A2.	
XX		
PD	20-NOV-1997.	
XX		
PE	13-MAY-1997;	97WO-US08101.
XX		
PR	18-FEB-1997;	97US-0800549.
PR	13-MAY-1996;	96US-0647577.

```
XX (HYBR-) HYBRIDON INC.
XX
XX 211man M;
XX
XX WPI; 1998-008873/01.
XX
XX New ribozyme variants having a shortened stem-loop II region - have
XX improved catalytic activity under low magnesium conditions and low
XX turnover conditions
XX
XX Disclosure; Page 51; 112pp; English.
XX
XX This is the nucleotide sequence of the PCR primer used for
XX amplification in the method of the invention which involves the
XX creation of ribozyme variants that have improved catalytic activity
XX under low magnesium condition. The ribozyme variant can be used to
XX cleave target RNA to control the expression of the RNA. They can be
XX used for treating diseases such as bacterial or viral infection, e.g.
XX HIV infection. They can also be used as RNA-specific restriction
XX endonucleases in the preparation of recombinant RNA molecules.
XX
XX Sequence 53 BP; 5 A; 13 C; 17 G; 18 T; 0 other;
SQ

Query Match          50.0%; Score 18; DB 19; Length 53;
Best Local Similarity 80.8%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 8 cttccaccatgagccagacacaccaa 33
   1 111111111111111111111111
Db 52 CGTGCACCATGACGACGACGCCA 27

RESULT 12
AAQ44724/c
ID AAQ44724 standard; DNA; 82 BP.
XX
XX AAQ44724;
AC
XX 18-OCT-1994 (first entry)
DT
XX
XX Oligonucleotide used to construct humanised antibody gene cassette.
DE
XX
XX Antibody: heavy chain; light chain; variable region; therapy;
KW constant region; prophylaxis; prevention; allergy; identification;
KW allergic reaction; immunoglobulin; IGE; determination; ss.
XX
XX Synthetic.
OS
XX EP589840-A.
PN
XX 30-MAR-1994.
PD
XX 15-SEP-1993; 93EP-0810653.
PF
XX 24-SEP-1992; 92GB-0020228.
PR 25-SEP-1992; 92US-0952802.
PS
XX (CIBA ) CIBA GEIGY AG.
PA (TANO-) TANOX BIOSYSTEMS INC.
PI Hardman N, Kolbinger F, Saldanha J;
XX
XX WPI; 1994-103410/13.
DR
XX
XX New reshaped human monoclonal antibody specific for IGE - used
XX for prophylaxis or treatment of allergic reactions or qualitative
XX or quantitative determ. of IGE
XX
XX Example 3; Page 51; 68pp; English.
PS
XX Reshaped human monoclonal antibodies can be used in the prophylaxis
CC
```

```
CC and/or treatment of allergic reactions in humans. The monoclonal
CC antibodies can also be used for the qualitative or quantitative
CC determination of IGE and for the determination of surface IGE
CC positive B cells. They can provide a long lasting therapeutic
CC effect without inducing immunogenicity as foreign proteins. Six
CC synthetic oligonucleotides (AAQ44719-24) were used to construct a
CC humanised antibody light chain variable region gene cassette.
XX
XX Sequence 82 BP; 11 A; 23 C; 23 G; 25 T; 0 other;
SQ

Query Match          50.0%; Score 18; DB 15; Length 82;
Best Local Similarity 80.8%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 11 ccaccatgagccagacaccaaagt 36
   111111111111111111111111
Db 60 CCACCTTCGCGCAGGACGACCAAGTG 35

RESULT 13
AAZ28558/c
ID AAZ28558 standard; DNA; 82 BP.
XX
XX AAZ28558;
AC
XX 24-DEC-1999 (first entry)
DT
XX
XX Oligonucleotide C21-LF for creating reshaped human antibody.
DE
XX
XX Diagnosis: IGE; immunoglobulin; body fluid; human; monoclonal antibody;
KW binding affinity; mouse; CDR; complementarity determining region;
KW allergy; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX US5958708-A.
PN
XX 28-SEP-1999.
PD
XX 07-JUN-1995; 95US-0476176.
PF
XX 27-SEP-1993; 93US-0127721.
PR 25-SEP-1992; 92US-0952802.
PS
XX (NOVS ) NOVARTIS CORP.
PA (TANO-) TANOX BIOSYSTEMS INC.
PI Saldanha J, Kolbinger F, Hardman N;
XX
XX WPI; 1999-570765/48.
DR
XX
XX new method for determining IGE levels in a sample
XX
XX Example 3; Column 55-56; 19pp; English.
PS
XX The invention relates to a method of determining IGE levels in a body
XX fluid sample, by contacting the sample with a reshaped human monoclonal
XX antibody (RA) having a binding affinity about equal to that of the
XX murine CDR-donor antibody TES-C21 produced by the cell line 11133.
XX The antibodies are useful in the diagnosis, prophylaxis and treatment
XX of allergy. Oligonucleotides AAZ28553-228564 are used to generate the
XX reshaped human antibodies AAZ28546-228552.
XX
XX Sequence 82 BP; 11 A; 23 C; 23 G; 25 T; 0 other;
SQ

Query Match          50.0%; Score 18; DB 20; Length 82;
Best Local Similarity 80.8%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 11 ccaccatgagccagacaccaaagt 36
```

```
||||| | ||||| ||||| |||
IDb 60 CCACCTTGCGCCAGGCGACCAAGATG 35

RESULT 14
AAI30004/C
ID AAI30004 standard; DNA; 31 BP.
XX
XX AAI30004;
AC
XX
XX 18-OCT-2001 (first entry)
DE
XX Human single nucleotide polymorphism (SNP) CPT2 4.
XX
XX Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Variation replace(16,C)
FT /tag=a
FT /standard_name="single nucleotide polymorphism"
XX
XX MO200166800-A2.
XX
XX 13-SEP-2001.
XX
XX 07-MAR-2001; 2001WO-US07268.
XX
XX 07-MAR-2000; 2000US-0187510.
XX
XX 22-MAY-2000; 2000US-0206129.
XX
XX (WHEB) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES;
XX
XX WPI; 2001-522952/57.
XX
XX Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype -
XX
XX Claim 1; Page 62; 145pp; English.
XX
XX The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
XX Sequence 31 BP; 7 A; 4 C; 7 G; 13 T; 0 other;
SQ

Query Match 48.9%; Score 17.6; DB 22; Length 31;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 ccacatgagccagcaccacaag 34
| | | | | | | | | | | | | | |
IDb 31 CCATCTTGATCCAGGACATCAAG 8

RESULT 15
ABA95305
ID ABA95305 standard; DNA; 36 BP.
XX
XX ABA95305;
AC
```

```
XX
XX 04-MAR-2002 (first entry)
DE
XX Human tyrosyl protein sulphotransferase, TPST-2, forward PCR primer.
XX
XX Human; TPST-2; PCR primer; autism; tyrosyl protein sulphotransferase;
KW digestive enzyme; food allergy; attention deficit disorder;
KW obsessive compulsive disorder; Crohn's disease; Coeliac disease;
KW dyspraxia; eating disorder; irritable bowel syndrome; schizophrenia;
KW schizoaffective disorder; ulcerative colitis; chronic fatigue syndrome;
KW Angelman's syndrome; rheumatic fever; Sydenham's chorea;
XX Tourette's syndrome; Prader Willi syndrome; tics; ss.
XX
XX Homo sapiens.
XX
XX MO200177681-A1.
XX
XX 18-OCT-2001.
XX
XX 05-APR-2001; 2001WO-GB01569.
XX
XX 06-APR-2000; 2000GB-0008326.
XX
XX (SHSI-) SHS INT LTD.
XX
XX Waring R, Phoenix J;
XX
XX WPI; 2002-010948/01.
XX
XX Detecting predisposition to autism and related diseases by detecting
PT reduced tyrosyl protein sulfoctransferase (TPST) activity and treating
PT those diseases by enhancing TPST or cholestyrolkin activity -
XX
XX Disclosure; Page 9; 42pp; English.
XX
XX The present invention relates to a method for detecting predisposition to
CC autism and related diseases. The method comprises assaying a sample in
CC vitro for reduced tyrosyl protein sulphotransferase (TPST) level compared
CC to a reference sample. TPST catalyses the transfer of sulphate from
CC 3'-phosphoadenosine 5'-phosphosulphate (PAPS) to tyrosine residues within
CC highly acidic regions of polypeptides. Autism-related diseases include
CC those associated with a 'leaky' gastrointestinal tract or inadequate
CC digestive enzymes leading to increased opioid activity, including gluten
CC or casein intolerance or food allergy, attention deficit disorder,
CC obsessive compulsive disorder, Crohn's disease, Coeliac disease,
CC particularly gluten-sensitive ataxics, dyspraxia, eating disorders such
CC as anorexia, irritable bowel syndrome, schizophrenia, schizoaffective
CC disorder and ulcerative colitis. Also related are those associated with
CC reduced CCK activity, including attention deficit hyperactivity disorder,
CC chronic fatigue syndrome and diseases commonly treated with dopamine
CC antagonists. Other diseases related to autism are those implicated as
CC genetically linked, including Angelman's syndrome, rheumatic fever,
CC Sydenham's chorea, Tourette's syndrome, Prader Willi syndrome and the
CC development of tics and diseases involving language problems. The present
CC sequence is a PCR primer, which can be used to amplify the entire open
CC reading frame (ORF) of human TPST-2 cDNA.
XX
XX Sequence 36 BP; 6 A; 9 C; 15 G; 6 T; 0 other;
SQ

Query Match 48.9%; Score 17.6; DB 24; Length 36;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ggcgaagcttcacatgagccag 24
| | | | | | | | | | | | | | |
IDb 1 ggcgaagcttcacatgagccagctg 24

Search completed: June 22, 2002, 05:39:59
Job time: 5074 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 04:14:30 ; Search time 98.05 Seconds
(Without alignments)
90.187 Million cell updates/sec

Title: US-09-927-267-12

Perfect score: 36

Sequence: 1 gcgaagctccacatgagccagacacaaagt 36

Scoring table: IDENTITY_NUC

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 613726

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :
1: Issued_Patents_MA:*
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5: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.2	53.3	34	2	US-08-765-783A-30
2	19.2	53.3	34	3	US-08-921-100-30
3	19.2	53.3	34	3	US-08-880-142-30
4	19.2	53.3	34	3	US-08-902-201-30
5	19.2	53.3	34	4	US-09-416-557-30
6	18.6	51.7	38	1	US-08-424-424B-5
7	18.6	51.7	55	4	US-08-483-511-14
8	18.6	51.7	55	5	PCT-US93-01009-14
9	18	50.0	82	2	US-08-476-176B-24
10	18	50.0	82	3	US-08-127-721A-24
11	17	47.2	82	3	US-08-485-246A-24
12	17	47.2	43	1	US-07-969-931-25
13	17	47.2	43	1	US-07-855-417A-25
14	17	47.2	96	1	US-08-479-783A-57
15	17	47.2	96	1	US-08-479-725-57
16	17	47.2	96	1	US-08-618-693-57
17	17	47.2	96	4	US-08-973-124-146
18	17	47.2	96	4	US-08-991-743C-57
19	17	47.2	96	5	PCT-US96-08014-146
20	16.8	46.7	31	5	PCT-US94-07091-1
21	16.8	46.7	35	4	US-08-848-760B-6
22	16.8	46.7	45	2	US-08-588-201-9
23	16.8	46.7	45	2	US-09-169-605-9
24	16.8	46.7	45	3	US-08-893-327-9
25	16.4	45.6	35	1	US-08-137-117D-40
26	16.4	45.6	35	1	US-08-436-717-40
27	16.2	45.0	30	3	US-08-557-210A-25

28	16.2	45.0	36	2	US-08-811-028-24	Sequence 24, Appl
29	16.2	45.0	36	2	US-08-811-028-25	Sequence 25, Appl
30	16	44.4	29	1	US-07-946-421-33	Sequence 33, Appl
31	16	44.4	36	1	US-08-137-117D-48	Sequence 48, Appl
32	16	44.4	36	1	US-08-436-717-48	Sequence 48, Appl
33	16	44.4	37	1	US-08-462-894-33	Sequence 43, Appl
34	16	44.4	37	1	US-08-206-185-33	Sequence 33, Appl
35	15.8	43.9	36	3	US-08-767-942A-37	Sequence 37, Appl
36	15.8	43.9	56	4	US-09-052-521C-31	Sequence 31, Appl
37	15.6	43.3	38	1	US-08-208-886C-69	Sequence 69, Appl
38	15.6	43.3	38	1	US-08-704-744-69	Sequence 69, Appl
39	15.6	43.3	52	1	US-08-427-097-22	Sequence 22, Appl
40	15.6	43.3	52	2	US-08-878-957-22	Sequence 22, Appl
41	15.4	42.8	34	4	US-08-646-265A-30	Sequence 30, Appl
42	15.2	42.2	28	1	US-08-487-753-10	Sequence 10, Appl
43	15.2	42.2	28	2	US-08-480-065-10	Sequence 10, Appl
44	15.2	42.2	28	3	US-08-487-744-10	Sequence 10, Appl
45	15.2	42.2	28	5	PCT-US93-09167-10	Sequence 10, Appl
46	15.2	42.2	29	2	US-08-143-311B-22	Sequence 22, Appl
47	15.2	42.2	30	4	US-09-277-457-9	Sequence 9, Appl
48	15.2	42.2	30	4	US-09-277-457-9	Sequence 21, Appl
49	15.2	42.2	47	2	US-08-467-603-68	Sequence 98, Appl
50	15.2	42.2	47	2	US-08-466-793-98	Sequence 98, Appl
51	15.2	42.2	47	2	US-08-491-861A-98	Sequence 98, Appl
52	15	41.7	34	3	US-08-836-561-14	Sequence 12, Appl
53	15	41.7	34	3	US-08-836-561-14	Sequence 12, Appl
54	15	41.7	36	1	US-08-137-117D-46	Sequence 46, Appl
55	15	41.7	36	1	US-08-436-717-46	Sequence 46, Appl
56	15	41.7	36	1	US-08-400-115-13	Sequence 46, Appl
57	15	41.7	37	2	US-08-765-783A-31	Sequence 13, Appl
58	15	41.7	37	3	US-08-921-100-31	Sequence 31, Appl
59	15	41.7	37	3	US-08-880-142-31	Sequence 31, Appl
60	15	41.7	37	3	US-08-902-201-31	Sequence 31, Appl
61	15	41.7	37	3	US-09-416-557-31	Sequence 31, Appl
62	15	41.7	41	3	US-08-718-728-7	Sequence 7, Appl
63	15	41.7	41	4	US-09-221-844-7	Sequence 7, Appl
64	15	41.7	41	5	PCT-US95-03323A-7	Sequence 7, Appl
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66	15	41.7	43	4	US-08-646-265A-32	Sequence 32, Appl
67	15	41.7	44	1	US-08-253-877C-44	Sequence 44, Appl
68	15	41.7	44	2	US-08-452-164A-44	Sequence 44, Appl
69	15	41.7	44	2	US-08-470-139-3	Sequence 3, Appl
70	15	41.7	44	4	US-08-569-147-25	Sequence 25, Appl
71	15	41.7	44	4	US-08-976-183A-20	Sequence 20, Appl
72	15	41.7	44	4	US-09-347-061-3	Sequence 3, Appl
73	15	41.7	58	1	US-08-146-422-22	Sequence 22, Appl
74	15	41.7	58	1	US-08-146-424-23	Sequence 23, Appl
75	15	41.7	58	1	US-08-466-865-2	Sequence 2, Appl
76	15	41.7	58	1	US-08-253-575-3	Sequence 3, Appl
77	15	41.7	58	1	US-08-626-554-4	Sequence 4, Appl
78	15	41.7	58	1	US-08-693-709-5	Sequence 5, Appl
79	14.8	41.1	26	1	US-08-010-997-7	Sequence 7, Appl
80	14.8	41.1	26	1	US-08-612-551-7	Sequence 7, Appl
81	14.8	41.1	26	2	US-09-006-232-7	Sequence 7, Appl
82	14.8	41.1	26	3	US-09-211-408-7	Sequence 7, Appl
83	14.8	41.1	30	5	PCT-US93-07672-7	Sequence 7, Appl
84	14.8	41.1	43	4	US-09-042-335-398	Sequence 398, Appl
85	14.8	41.1	43	4	US-08-758-417A-248	Sequence 248, Appl
86	14.8	41.1	62	4	US-08-483-511-13	Sequence 13, Appl
87	14.8	41.1	62	5	PCT-US93-01009-13	Sequence 13, Appl
88	14.8	41.1	69	4	US-08-591-632-71	Sequence 71, Appl
89	14.6	40.6	26	2	US-08-859-998-301	Sequence 301, Appl
90	14.6	40.6	26	4	US-09-223-928-101	Sequence 301, Appl
91	14.6	40.6	27	4	US-08-584-040-3186	Sequence 3186, Appl
92	14.6	40.6	28	2	US-08-137-9900A-20	Sequence 20, Appl
93	14.6	40.6	31	4	US-08-676-645-338	Sequence 338, Appl
94	14.6	40.6	31	4	US-09-194-285-48	Sequence 48, Appl
95	14.6	40.6	39	4	US-08-849-602C-22	Sequence 22, Appl
96	14.6	40.6	60	3	US-08-911-894-59	Sequence 59, Appl
97	14.6	40.6	85	1	US-08-447-169A-159	Sequence 159, Appl
98	14.4	40.0	20	2	US-08-765-783A-70	Sequence 70, Appl
99	14.4	40.0	20	3	US-08-921-100-70	Sequence 70, Appl
100	14.4	40.0	20	3	US-08-880-142-20	Sequence 20, Appl

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C 979 12.2 33.9 78 1 US-08-400-256-11
C 980 12.2 33.9 78 2 US-09-073-033-6
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C 982 12.2 33.9 80 2 US-08-116-778E-23
C 983 12.2 33.9 80 2 US-08-438-562-23
C 984 12.2 33.9 80 2 US-08-483-528B-23
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C 986 12.2 33.9 81 1 US-08-287-001A-5
C 987 12.2 33.9 81 3 US-08-921-887-38
C 988 12.2 33.9 81 5 PCT-US95-09941-5
C 989 12.2 33.9 86 4 US-09-564-805-17
C 990 12.2 33.9 87 1 US-08-110-286A-3
C 991 12.2 33.9 90 1 US-08-488-144-20
C 992 12.2 33.9 90 4 US-08-974-549A-691
C 993 12.2 33.9 90 4 US-08-974-549A-692
C 994 12.2 33.9 90 4 US-08-464-700-45
C 995 12.2 33.9 93 3 US-08-976-413A-422
C 996 12.2 33.9 94 2 US-08-483-528B-57
C 997 12.2 33.9 94 3 US-08-673-799C-57
C 998 12.2 33.9 95 1 US-08-180-195-16
C 999 12.2 33.9 95 1 US-08-180-195-17
1000 12.2 33.9 95 1 US-08-477-329-16

ALIGNMENTS

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Sequence 11, Appl
Sequence 6, Appl
Sequence 11, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 5, Appl
Sequence 38, Appl
Sequence 5, Appl
Sequence 17, Appl
Sequence 3, Appl
Sequence 20, Appl
Sequence 691, App
Sequence 692, App
Sequence 45, Appl
Sequence 422, App
Sequence 57, Appl
Sequence 57, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 16, Appl

RESULT 1
US-08-765-783A-30
; Sequence 30, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765.783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs

TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1..34
; OTHER INFORMATION: chvL backward primer
US-08-765-783A-30

Query Match 53.3%; Score 19.2; DB 2; Length 34;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4 aaagcttcaccatgacgacgacccaagt 35
|||||
Db 3 AAAGCTTCACCATGAGTGTCTACTCAGGT 34

RESULT 2
US-08-921-100-30
; Sequence 30, Application US/08921100
; Patent No. 6024956
; GENERAL INFORMATION:
; APPLICANT: MATSUSHIMA, KOUJI
; APPLICANT: MATSUMOTO, YOSHIHIRO
; APPLICANT: YAMADA, YOSHIKI
; APPLICANT: SATO, KOH
; APPLICANT: TSUCHIYA, MASSAYUKI
; APPLICANT: YAMAZAKI, TATSUMI
; TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921.100
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,323
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 15580-0001.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-921-100-30

Query Match 53.3%; Score 19.2; DB 3; Length 34;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 4 aaagcttcaccatgacgacgacccaagt 35

Db 3 AAAGCTTCACCATGAGTGCTCAGT 34

RESULT 3
US-08-880-142-30
Sequence 30, Application US/08880142
Patent No. 6048972
GENERAL INFORMATION:
APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: MATSUMOTO, YOSHIHIRO
APPLICANT: YAMADA, YOSHIKI
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI
TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. NW, Suite 5500
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,142
FILING DATE: 20-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/345,145
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 15580-0001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-880-142-30

Query Match 53.3%; Score 19.2; DB 3; Length 34;
Best Local Similarity 75.0%; Pred. NO. 27;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 3 AAAGCTTCACCATGAGTGCTCAGT 34

RESULT 4
US-08-902-201-30
Sequence 30, Application US/08902201
Patent No. 6068840
GENERAL INFORMATION:
APPLICANT: MATSUSHIMA, KOUJI
APPLICANT: MATSUMOTO, YOSHIHIRO
APPLICANT: YAMADA, YOSHIKI
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, MASSAYUKI
APPLICANT: YAMAZAKI, TATUMI

TITLE OF INVENTION: HUMANIZED ANTI-IL8 ANTIBODY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. NW, Suite 5500
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,201
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/437,328
FILING DATE: 09-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 15580-0001.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-902-201-30

Query Match 53.3%; Score 19.2; DB 3; Length 34;
Best Local Similarity 75.0%; Pred. NO. 27;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 3 AAAGCTTCACCATGAGTGCTCAGT 34

RESULT 5
US-09-416-557-30
Sequence 30, Application US/09416557
Patent No. 6245894
GENERAL INFORMATION:
APPLICANT: Matsushima, Kouji
APPLICANT: Matsumoto, Yoshihiro
APPLICANT: Yamada, Yoshiki
APPLICANT: Sato, Koh
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 5

RESULT 8

REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-127-721A-24

Query Match 50.0%; Score 18; DB 3; Length 82;
Best Local Similarity 80.8%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 11 ccacatgagcagagaccacaaagt 36
||||| |
DB 60 CCACCTTCGCGCAGGCGCACCAGGTG 35

RESULT 11
US-08-485-246A-24/C
Sequence 24, Application US/08485246A
Patent No. 6072035
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldana, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF SEQUENCES: 55
TITLE OF INVENTION: Immunoglobulin isotype
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6072035artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-485-246A-24

Query Match 50.0%; Score 18; DB 3; Length 82;

Best Local Similarity 80.8%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 11 ccacatgagcagagaccacaaagt 36
||||| |
DB 60 CCACCTTCGCGCAGGCGCACCAGGTG 35

RESULT 12
US-07-969-931-25
Sequence 25, Application US/07969931
Patent No. 5458874
GENERAL INFORMATION:
APPLICANT: Pereira, Heloise Anne
APPLICANT: Spitznagel, John K.
TITLE OF INVENTION: Chemotactic, Antibiotic and
TITLE OF INVENTION: Lipopolysaccharide-Binding Peptide Fragments of CAP37
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Needle & Rosenberg, P.C.
STREET: 133 Carnegie Way N.W., Suite 400
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,931
FILING DATE: 19921030
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/543,151
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/375,739
FILING DATE: 05-JUL-1989
ATTORNEY/AGENT INFORMATION:
NAME: Severson, Mary L.
REGISTRATION NUMBER: 34,927
REFERENCE/DOCKET NUMBER: 0510.024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-969-931-25

Query Match 47.2%; Score 17; DB 1; Length 43;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 aagcttcacatgagcagacac 29
||||| |
DB 11 AAGCTTCACATGAGCCGCGTGAC 35

RESULT 13
US-07-855-417A-25
Sequence 25, Application US/07855417A
Patent No. 5484885
GENERAL INFORMATION:
APPLICANT: Pereira, Heloise Anne
APPLICANT: Spitznagel, John K.

TITLE OF INVENTION: Chemotactic, Antibiotic and
NUMBER OF INVENTION: Lipopolysaccharide-Binding Peptide Fragments of CAP37
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Needie & Rosenberg, P.C.
STREET: 133 Carnegie Way N.W., Suite 400
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/855,417A
FILING DATE: 18-MAR-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/543,151
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/375,739
FILING DATE: 05-JUL-1989
ATTORNEY/AGENT INFORMATION:
NAME: Severson, Mary L.
REGISTRATION NUMBER: 34,927
REFERENCE/DOCKET NUMBER: 0510,024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-855-417A-25

Query Match 47.2%; Score 17; DB 1; Length 43;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 aagcttcaccatgagccagacac 29
DB 11 AAGCTTCACCATGACCGCGGTGAC 35

RESULT 14
US-08-479-783A-57
Sequence 57, Application US/08479783A
Patent No. 5668264
GENERAL INFORMATION:
APPLICANT: NEBOUSA JANJIC
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
OPERATING SYSTEM: IBM compatible
SOFTWARE: WordPerfect 5.1
APPLICATION NUMBER: US/08/479,725

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,783A
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX42-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-F
US-08-479-783A-57

Query Match 47.2%; Score 17; DB 1; Length 96;
Best Local Similarity 68.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 gaaagcttcaccatgagccagac 27
DB 41 GACAGCUUUGACCAUGAGCUGGAC 65

RESULT 15
US-08-479-725-57
Sequence 57, Application US/08479725
Patent No. 5674685
GENERAL INFORMATION:
APPLICANT: NEBOUSA JANJIC
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
OPERATING SYSTEM: IBM compatible
SOFTWARE: WordPerfect 5.1
APPLICATION NUMBER: US/08/479,725
FILING DATE: 7-JUNE-1995

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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McLearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX42-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-F
; OTHER INFORMATION: modified
US-08-479-725-57

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Query Match      47.2%; Score 17; DB 1; Length 96;
Best Local Similarity 68.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      3 gaaagcttcaccatgacgagac 27
        |||||: ||||| ||||
DB      41 GACAGCCTUUGACCAUGAGCUGGAC 65

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Search completed: June 22, 2002, 05:33:31
 Job time: 4741 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 04:05:40 ; Search time 2443.9 Seconds
(without alignments) 198.818 Million cell updates/sec

Title: US-09-927-267-12
Perfect score: 36
Sequence: 1 gcgaagctccacatgacgacgacacaaagt 36

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 297742

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlu: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_estl: *
10: gb_est2: *
11: gb_hlc: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pln: *
16: em_gss_vrt: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	48.9	61	10	BE571706
2	17.6	48.9	64	10	AA256029
3	17.4	48.3	70	12	TA386B04
4	17.4	48.3	77	9	AI158677
5	16.8	46.7	58	9	AI023530
6	16.8	46.7	66	12	A2328396
7	16	44.4	62	10	F24048
8	16	44.4	62	12	CNS03D7C
9	16	44.4	85	12	A2920865
10	16	44.4	93	9	AA062074
11	15.8	43.9	71	12	A2499552
12	15.8	43.9	80	10	R46756
13	15.6	43.3	43	10	BI197684
14	15.6	43.3	43	10	BF311795
15	15.6	43.3	43	10	BF312493
16	15.6	43.3	43	10	BF315164
17	15.6	43.3	70	10	BG503868

18	15.6	43.3	73	10	BE228766
19	15.6	43.3	74	12	BH226010
20	15.6	43.3	79	9	AA587583
21	15.4	42.8	63	9	AV833733
22	15.4	42.8	70	9	AI089535
23	15.4	42.8	78	9	AA674932
24	15.4	42.8	84	9	AA113951
25	15.4	42.8	95	10	BF178449
26	15.2	42.2	64	9	AA013549
27	15.2	42.2	82	9	AI679682
28	15.2	42.2	94	12	BSA275789
29	15.2	42.2	96	9	AM307064
30	15.2	42.2	98	10	T61786
31	15.2	42.2	100	12	A2785459
32	15.2	42.2	100	12	A2785459
33	15.2	41.7	53	10	A2411328
34	15.2	41.7	53	10	BI091807
35	15.2	41.7	79	12	BI1794
36	15.2	41.7	85	9	AI545056
37	15.2	41.7	85	10	T60481
38	15.2	41.7	92	10	D12094
39	15.2	41.7	96	9	AI414856
40	15.2	41.7	97	9	AA633275
41	15.2	41.7	98	10	BI862877
42	15.2	41.7	98	10	BI862877
43	15.2	41.7	100	10	BF946786
44	14.8	41.1	34	9	AA779194
45	14.8	41.1	49	10	BE282036
46	14.8	41.1	60	12	A2609301
47	14.8	41.1	69	9	AA551533
48	14.8	41.1	73	10	AA934094
49	14.8	41.1	73	10	W83192
50	14.8	41.1	73	12	TA61B09P
51	14.8	41.1	74	9	AA246231
52	14.8	41.1	79	9	AA731299
53	14.8	41.1	80	10	D19080
54	14.8	41.1	83	9	AA532978
55	14.8	41.1	87	12	A2600429
56	14.8	41.1	87	12	A2600429
57	14.8	41.1	88	10	F37888
58	14.8	41.1	88	12	A2788938
59	14.8	41.1	89	10	BM284162
60	14.8	41.1	91	9	AA077122
61	14.8	41.1	93	10	H86708
62	14.8	41.1	96	9	AI955343
63	14.8	41.1	100	10	BG209819
64	14.6	40.6	35	12	A2763763
65	14.6	40.6	35	12	A2763763
66	14.6	40.6	37	12	A2763763
67	14.6	40.6	46	12	A2793780
68	14.6	40.6	54	12	A2796113
69	14.6	40.6	72	10	BG151288
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71	14.6	40.6	81	10	BE891840
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73	14.6	40.6	84	12	A2787015
74	14.6	40.6	91	9	AI957617
75	14.6	40.6	92	12	A2606696
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77	14.6	40.6	98	9	AA458451
78	14.6	40.6	98	9	AA026309
79	14.4	40.0	48	10	N57213
80	14.4	40.0	51	12	A2808470
81	14.4	40.0	53	9	AV852307
82	14.4	40.0	53	10	BG235568
83	14.4	40.0	55	10	BG231022
84	14.4	40.0	60	10	BG271430
85	14.4	40.0	61	10	W95439
86	14.4	40.0	69	9	AA930101
87	14.4	40.0	73	9	AA191061
88	14.4	40.0	77	2	HSM003312
89	14.4	40.0	78	10	T74784
90	14.4	40.0	79	12	A2474270

C 967 12.4 34.4 95 9 A1638790 tt32d03.x
C 968 12.4 34.4 95 10 U38154 OSU38154.FD
C 969 12.4 34.4 95 10 BE889215
C 970 12.4 34.4 95 12 BH223299
C 971 12.4 34.4 96 9 AA890109
C 972 12.4 34.4 96 9 AA127992
C 973 12.4 34.4 96 9 AA172804
C 974 12.4 34.4 96 10 BM437656
C 975 12.4 34.4 97 9 AA064274
C 976 12.4 34.4 97 9 AA641181
C 977 12.4 34.4 97 9 AA732691
C 978 12.4 34.4 97 9 AA868913
C 979 12.4 34.4 97 9 AA874635
C 980 12.4 34.4 97 9 AA897326
C 981 12.4 34.4 97 9 AA147075
C 982 12.4 34.4 97 9 AA1817510
C 983 12.4 34.4 97 9 AA198324
C 984 12.4 34.4 97 10 BG302506
C 985 12.4 34.4 97 10 B1138472
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C 988 12.4 34.4 98 10 BG252746
C 989 12.4 34.4 98 10 BG428177
C 990 12.4 34.4 98 10 BE324473
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C 992 12.4 34.4 99 9 AA887398
C 993 12.4 34.4 99 9 AA1451320
C 994 12.4 34.4 99 9 AV841556
C 995 12.4 34.4 99 10 H57347
C 996 12.4 34.4 99 10 W33923
C 997 12.4 34.4 100 9 AA061960
C 998 12.4 34.4 100 9 AA935102
C 999 12.4 34.4 100 9 AA1320142
C1000 12.4 34.4 100 9 AA206256

ALIGNMENTS

RESULT 1
LOCUS BE571706 61 bp mRNA linear EST 15-AUG-2000
DEFINITION 601330055f1 NCI_CGAP_Mam6 Mus musculus CDNA clone IMAGE:3707725 5',
mRNA sequence.
ACCESSION BE571706
VERSION BE571706.1 GI:9815426
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 61)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM8925 row: n column: 14
High quality sequence stop: 61.
Location/Qualifiers

FEATURES
Source 1..61
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3707725"
/clone_lib="NCI_CGAP_Mam6"

/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-Sport6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies, Inc. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 28 a 15 c 9 g 9 t

ORIGIN

Query Match 48.9%; Score 17.6; DB 10; Length 61;
Best Local Similarity 71.9%; Pred. No. 6.3e+03;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 4 aaagcttcacatagccagcaccacaaagt 35
Db 20 ATACTCACACCATATCCAGCATACAAAGT 51

RESULT 2
LOCUS AA256029 64 bp mRNA linear EST 13-AUG-1997
DEFINITION zs28f01.r1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:686521 5',
sequence.
ACCESSION AA256029
VERSION AA256029.1 GI:1891569
KEYWORDS EST.
SOURCE human.
ORGANISM human
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 64)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Insert length: 619 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

Source 1..64
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:686521"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+ IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAAGGAGCGGCGCCCTCATTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT3D vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 23 a 16 c 11 g 14 t

REFERENCE	Mammalia: Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 77) Marra,M., Haller,T., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Weising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse Est Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:920681 Trace considered overall poor quality Seq primer: -26ml3 rev2 ET from Amersham High quality sequence stop: 1. Location/Qualifiers
FEATURES	source 1..77 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone_image="1447365" /clone_id="Soares_mammary_gland_Nbmwg" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /note="Organ: mammary gland; Vector: pT7T3D-Pac (pharmacia RI, 1st strand cDNA was primed with a Not I - o11go(dT) primer [5'] TGTTACCAATCTGAAGTGGAGCGCCGCGCAATGTGTTTTTTTTTTTTTTTTTTT T 3.); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldoo."
BASE COUNT	17 a 15 c 29 g 16 t
ORIGIN	
Query Match	48.3%; Score 17.4; DB 9; Length 77;
Best Local Similarity	77.8%; Pred. No. 8.1e+03;
Matches 21; Conservative %;	0; Mismatches 6; Indels 0; Gaps 0;
CY	9 ttccaccatgagccagcaccaagt 35
DB	48 TGCTTCATGAGCGAAGTCACCACACT 22
RESULT 5	
A1023530/c	
LOCUS	A1023530 58 bp mRNA linear EST 27-AUG-1998
DEFINITION	ov79d08.s1 Soares_testis.NHT Homo sapiens CDNA clone IMAGE:1643535
3' similar to SW:NIAM_BOVIN_002312 NADH-UBIQUINONE OXIDOREDUCTASE	
ASHI SUBUNIT PRECURSOR ; , mRNA sequence.	
ACCESSION	A1023530
KEYWORDS	A1023530.1 GI:3238574
SOURCE	EST.
ORGANISM	Homo sapiens human.
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini; Homnidae; Homo.
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
TITLE	

BASE COUNT	21 a	22 c	11 g	7 t	1 others
ORIGIN					
Query Match	44.4%	Score 16;	DB 12;	Length 62;	
Best Local Similarity	79.2%	Pred. No. 2.6e+04;			
Matches 19;	Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;
QY	8	ctccaccatgagccagacacca 31			
Db	25	CTCACACATCATCTCCAGACACCA 48			
RESULT	9				
AZ920865		85 bp	DNA	linear	GSS 17-DEC-2001
LOCUS					
DEFINITION	1006021F02.2EL_x1 1006 - Rescuemu Grid G zea mays genomic, DNA				
ACCESSION	AZ920865				
VERSION	AZ920865.1	GI:13391727			
KEYWORDS	GSS.				
SOURCE	zea mays.				
ORGANISM	zea mays.				
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 85)				
TITLE	Walbot.V.				
JOURNAL	Maize genomic sequences found using engineered Rescuemu transposon				
COMMENT	Unpublished (2001)				
	Contact: Walbot V				
	Department of Biological Sciences				
	Stanford University				
	855 California Ave, Palo Alto, CA 94304, USA				
	Tel: 650 723 2227				
	Fax: 650 725 8221				
	Email: walbot@stanford.edu				
	Possible ligation site of ends cut by 2 different endonucleases.				
	Reverse complemented post-ligation sequence from source sequence.				
	Plate: 1006021 row: 38				
	Class: transposon-tagged.				
FEATURES	Location/Qualifiers				
source	1..85				
	/organism="Zea mays"				
	/cultivar="mixed background W23/A188/B73"				
	/db_xref="taxon:4577"				
	/clone_lib="1006 - Rescuemu Grid G"				
	/tissue_type="leaf"				
	/dev_stage="adult"				
	/lab_host="DH10B"				
	/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site.1: BamHI; Site.2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."				
BASE COUNT	21 a	27 c	27 g	10 t	
ORIGIN					
Query Match	44.4%	Score 16;	DB 12;	Length 85;	
Best Local Similarity	79.2%	Pred. No. 2.9e+04;			
Matches 19;	Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

BASE COUNT	21 a	22 c	11 g	7 t	1 others
ORIGIN					
Query Match	44.4%	Score 16;	DB 12;	Length 62;	
Best Local Similarity	79.2%	Pred. No. 2.6e+04;			
Matches 19;	Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;
QY	8	ctccaccatgagccagacacca 31			
Db	25	CTCACACATCATCTCCAGACACCA 48			
RESULT	9				
AZ920865		85 bp	DNA	linear	GSS 17-DEC-2001
LOCUS					
DEFINITION	1006021F02.2EL_x1 1006 - Rescuemu Grid G zea mays genomic, DNA				
ACCESSION	AZ920865				
VERSION	AZ920865.1	GI:13391727			
KEYWORDS	GSS.				
SOURCE	zea mays.				
ORGANISM	zea mays.				
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 85)				
TITLE	Walbot.V.				
JOURNAL	Maize genomic sequences found using engineered Rescuemu transposon				
COMMENT	Unpublished (2001)				
	Contact: Walbot V				
	Department of Biological Sciences				
	Stanford University				
	855 California Ave, Palo Alto, CA 94304, USA				
	Tel: 650 723 2227				
	Fax: 650 725 8221				
	Email: walbot@stanford.edu				
	Possible ligation site of ends cut by 2 different endonucleases.				
	Reverse complemented post-ligation sequence from source sequence.				
	Plate: 1006021 row: 38				
	Class: transposon-tagged.				
FEATURES	Location/Qualifiers				
source	1..85				
	/organism="Zea mays"				
	/cultivar="mixed background W23/A188/B73"				
	/db_xref="taxon:4577"				
	/clone_lib="1006 - Rescuemu Grid G"				
	/tissue_type="leaf"				
	/dev_stage="adult"				
	/lab_host="DH10B"				
	/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site.1: BamHI; Site.2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."				
BASE COUNT	21 a	27 c	27 g	10 t	
ORIGIN					
Query Match	44.4%	Score 16;	DB 12;	Length 85;	
Best Local Similarity	79.2%	Pred. No. 2.9e+04;			
Matches 19;	Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

OY 1 gccgaagcttcaccatgagccag 24
 ||||||| ||| | |||||||
 Db 59 gccgaagcaaccagccagccag 82

RESULT 10

AA062074/c 93 bp mRNA linear EST 23-SEP-1996
 LOCUS mJ8f12.r1 Soares mouse p3MNF19.5 Mus musculus cDNA clone

DEFINITION IMAGE:482735 5' similar to gb:219054 BETA-CATENIN (HUMAN);
 gb:M90364 Mouse (MOUSE);, mRNA sequence.

ACCESSION AA062074
 VERSION AA062074.1 GI:1555873
 KEYWORDS EST.

SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 93)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Scheinberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterson,R.

TITLE The WashU-HMT Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMT Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:293479
 Trace considered overall poor quality
 Seg primer: -28M13 rev2 from Amersham
 High quality sequence stop: 1.

FEATURES
 Source location/Qualifiers

1..93
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:482735"
 /clone_lib="Soares mouse p3MNF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pT7T3D (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer; 15',
 TGTTCACATCTGAGTGGAGCGCGCATTTTCTTTTCTTTT 3',
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Patima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."

HASE COUNT 13 a 15 c 41 g 24 t
 ORIGIN

Query Match 44.4%; Score 16; DB 9; Length 93;
 Best Local Similarity 79.2%; Pred. No. 2.9e+04;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 9 ttccacatgagccagcagaccacaa 32
 | ||||| ||| ||| |||||||
 Db 93 tcccaagatcagcagcagaccacaa 70

RESULT 11
 A2499552/c

LOCUS A2499552 71 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0337H19F Mouse 10kb plasmid U0GC1M library Mus musculus genomic
 clone U0GC1M0337H19 F, DNA sequence.

ACCESSION A2499552
 VERSION A2499552.1 GI:10678493
 KEYWORDS GSS.

SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 71)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
 and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0337 row: H column: 19
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 71.

FEATURES
 Source location/Qualifiers

1..71
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U0GC1M0337H19"
 /clone_lib="Mouse 10kb plasmid U0GC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/nares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (911473211419b1AF129072.1), a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 16 a 15 c 17 g 23 t
 ORIGIN

Query Match 43.9%; Score 15.8; DB 12; Length 71;
 Best Local Similarity 74.1%; Pred. No. 3.2e+04;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 8 ctccacatgagccagcagaccacaa 34
 | ||||||| ||| | |||||||
 Db 69 cttccacatgagccagcagaccacaa 43

RESULT 12

R46756/c 80 bp mRNA linear EST 10-MAY-1995
LOCUS yj54b02.s1 Soares breast 2NbHst Homo sapiens cDNA clone
IMAGE:152523 3', mRNA sequence.
ACCESSION R46756
VERSION R46756.1 GI:806153
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 80)
AUTHORS Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 811
High quality sequence stops: 59 Source: IMAGE Consortium, LNL. This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 811 Std Error: 0.00
Seq Primer: Promega -21m13
High quality sequence stop: 59.
Location/Qualifiers
1..80
/organism="Homo sapiens"
/db_xref="GDB:564740"
/db_xref="taxon:9606"
/clone="IMAGE:152523"
/clone_lib="Soares breast 2NbHst"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: breast; Vector: pRT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGAGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonalido."
BASE COUNT 21 a 24 c 15 g 19 t 1 others
ORIGIN

Query Match 43.9%; Score 15.8; DB 10; Length 80;
Best Local Similarity 74.1%; Pred. No. 3.3e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 7 gcttcacatgagcagacaccaa 33
||||| ||||| ||||| ||
Db 44 gcttctaccatgacgacgacattaa 18

RESULT 13
B1197684 43 bp mRNA linear EST 10-JUL-2001
LOCUS B1197684
DEFINITION 602757596F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4893191 5',
mRNA sequence.
ACCESSION B1197684
VERSION B1197684.1 GI:14652704
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L1CM1774 row: p column: 24
High quality sequence stop: 43.
Location/Qualifiers
1..43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4893191"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOT87; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
BASE COUNT 6 a 12 c 15 g 10 t
ORIGIN

Query Match 43.3%; Score 15.6; DB 10; Length 43;
Best Local Similarity 70.0%; Pred. No. 3.2e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 3 gaagcttcacatgagcagacaccaa 32
||||| ||||| ||||| ||
Db 37 GAACGGCTCTCCAGATCCGTAGACCAA 8

RESULT 14
BF311795 43 bp mRNA linear EST 21-NOV-2000
LOCUS BF311795
DEFINITION 601897304F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126512 5',
mRNA sequence.
ACCESSION BF311795
VERSION BF311795.1 GI:11259557
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L1CM1016 row: h column: 01
High quality sequence stop: 43.
Location/Qualifiers

Source

```

SOURCE
1. .43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image:4126512"
/clone_lib="NH_MGC_19"
/lisuse_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/notes=Organ: brain; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NH_MGC Library."
BASE COUNT
6 a 12 c 15 g 10 t

```

BASE COUNT
ORIGIN

6 a 12 c 15 g 10 t

Query Match

Best Local Similarity 70.0%; Pred. No. 3.2e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0;
Gaps 0

```

2y      3  gaaagcttcaccatgagccagacaccaa 32
      ||| | ||| | ||| | ||| |
db      37  GAACGGCTCCTCCAGATCCCGTAGACCA 8

```

RESULT 15
3F312493/C

LOCUS	BF312493	43 bp	mRNA	linear	EST 21-NOV-2000
DEFINITION	601897453f1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126932 5',				

ORGANISM

REFERENCE
AUTHORS
NIH-MGC <http://mgc.ncl.nih.gov/>.
1 (bases 1 to 43)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

(COMMENT)

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: [McG clone distribution](#) information can be found through the I.M.A.G.E. Consortium/[LIND](#) at: [image.lind.gov](#)
 Plate: [LICM1017](#) row: 1 column: 13
 High quality sequence stop: 43.

FEATURES

source

Location/Qualifiers
1. .43

EASE COUNT

6 a 12 c 15 g 10 e

Query Match	43.38;	Score 15.6;	DB 10;	Length 43;
Best Local Similarity	70.08;	Pred..No. 3.2e+04;		
Matches 21; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;

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QY      3  gaaagcttcacccatgagccagacaccaa 32
          ||| | ||| ||| ||| ||| |||
Db      37  GAACGGCTCCTCCAGGATCCCGTAGACCAA 8

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Search completed: June 22, 2002, 04:59:26
Job time: 3226 sec

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